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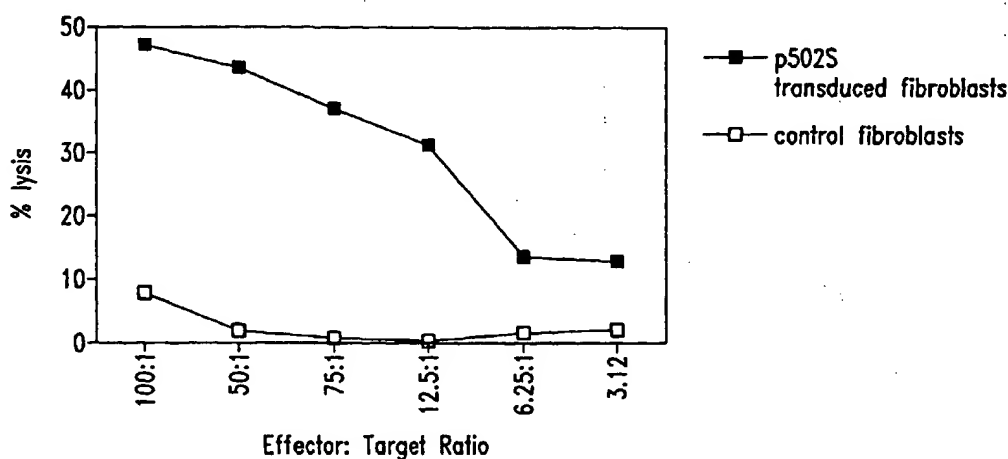
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- (71) Applicant (*for all designated States except US*): CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): XU, Jiangchun [US/US]; 15805 SE 43rd Place, Bellevue, WA 98006 (US). SKEIKY, Yasir, A., W. [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006 (US). REED, Steven, G. [US/US]; 2843 - 122nd Place NE, Bellevue, WA 98005 (US). CHEEVER, Martin, A. [US/US]; 6210 Southeast 22nd, Mercer Island, WA 98040 (US).
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(54) Title: COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER



(57) Abstract: Compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer, are disclosed. Compositions may comprise one or more prostate tumor proteins, immunogenic portions thereof, or polynucleotides that encode such portions. Alternatively, a therapeutic composition may comprise an antigen presenting cell that expresses a prostate tumor protein, or a T cell that is specific for cells expressing such a protein. Such compositions may be used, for example, for the prevention and treatment of diseases such as prostate cancer. Diagnostic methods based on detecting a prostate tumor protein, or mRNA encoding such a protein, in a sample are also provided.

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COMPOSITIONS AND METHODS FOR THERAPY AND DIAGNOSIS OF PROSTATE CANCER

TECHNICAL FIELD

The present invention relates generally to therapy and diagnosis of cancer, such as prostate cancer. The invention is more specifically related to polypeptides comprising at least a portion of a prostate tumor protein, and to polynucleotides encoding such polypeptides. Such polypeptides and polynucleotides may be used in vaccines and pharmaceutical compositions for prevention and treatment of prostate cancer, and for the diagnosis and monitoring of such cancers.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

In spite of considerable research into therapies for these and other cancers, prostate cancer remains difficult to diagnose and treat effectively. Accordingly, there is a need in the art for improved methods for detecting and treating

such cancers. The present invention fulfills these needs and further provides other related advantages.

SUMMARY OF THE INVENTION

Briefly stated, the present invention provides compositions and methods for the diagnosis and therapy of cancer, such as prostate cancer. In one aspect, the present invention provides polypeptides comprising at least a portion of a prostate tumor protein, or a variant thereof. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments, the polypeptide comprises at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; (b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and (c) complements of any of the sequence of (a) or (b). In certain specific embodiments, such a polypeptide comprises at least a portion, or variant thereof, of a tumor protein that includes an amino acid sequence selected from the group consisting of sequences recited in any one of SEQ ID NO: 112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a prostate tumor protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, vaccines are provided. Such vaccines comprise a polypeptide or polynucleotide as described above and a non-specific immune response enhancer.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a prostate tumor protein; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a non-specific immune response enhancer.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides encoding such fusion proteins.

Within related aspects, pharmaceutical compositions comprising a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a physiologically acceptable carrier are provided.

Vaccines are further provided, within other aspects, that comprise a fusion protein, or a polynucleotide encoding a fusion protein, in combination with a non-specific immune response enhancer.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient a pharmaceutical composition or vaccine as recited above.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of a prostate tumor protein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer in a patient, comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody. The cancer may be prostate cancer.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount

detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 illustrates the ability of T cells to kill fibroblasts expressing the representative prostate tumor polypeptide P502S, as compared to control fibroblasts. The percentage lysis is shown as a series of effector:target ratios, as indicated.

Figures 2A and 2B illustrate the ability of T cells to recognize cells expressing the representative prostate tumor polypeptide P502S. In each case, the number of γ -interferon spots is shown for different numbers of responders. In Figure 2A, data is presented for fibroblasts pulsed with the P2S-12 peptide, as compared to fibroblasts pulsed with a control E75 peptide. In Figure 2B, data is presented for fibroblasts expressing P502S, as compared to fibroblasts expressing HER-2/*neu*.

Figure 3 represents a peptide competition binding assay showing that the P1S#10 peptide, derived from P501S, binds HLA-A2. Peptide P1S#10 inhibits HLA-A2 restricted presentation of fluM58 peptide to CTL clone D150M58 in TNF release bioassay. D150M58 CTL is specific for the HLA-A2 binding influenza matrix peptide fluM58.

Figure 4 illustrates the ability of T cell lines generated from P1S#10 immunized mice to specifically lyse P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat A2Kb targets, as compared to EGFP-transduced Jurkat A2Kb. The percent lysis is shown as a series of effector to target ratios, as indicated.

Figure 5 illustrates the ability of a T cell clone to recognize and specifically lyse Jurkat A2Kb cells expressing the representative prostate tumor polypeptide P501S, thereby demonstrating that the P1S#10 peptide may be a naturally processed epitope of the P501S polypeptide.

Figures 6A and 6B are graphs illustrating the specificity of a CD8⁺ cell line (3A-1) for a representative prostate tumor antigen (P501S). Figure 6A shows the results of a ⁵¹Cr release assay. The percent specific lysis is shown as a series of effector:target ratios, as indicated. Figure 6B shows the production of interferon-gamma by 3A-1 cells stimulated with autologous B-LCL transduced with P501S, at varying effector:target ratios as indicated.

SEQ ID NO: 1 is the determined cDNA sequence for F1-13

SEQ ID NO: 2 is the determined 3' cDNA sequence for F1-12

SEQ ID NO: 3 is the determined 5' cDNA sequence for F1-12

SEQ ID NO: 4 is the determined 3' cDNA sequence for F1-16

SEQ ID NO: 5 is the determined 3' cDNA sequence for H1-1

SEQ ID NO: 6 is the determined 3' cDNA sequence for H1-9

SEQ ID NO: 7 is the determined 3' cDNA sequence for H1-4

SEQ ID NO: 8 is the determined 3' cDNA sequence for J1-17

SEQ ID NO: 9 is the determined 5' cDNA sequence for J1-17

SEQ ID NO: 10 is the determined 3' cDNA sequence for L1-12

SEQ ID NO: 11 is the determined 5' cDNA sequence for L1-12

SEQ ID NO: 12 is the determined 3' cDNA sequence for N1-1862

SEQ ID NO: 13 is the determined 5' cDNA sequence for N1-1862

SEQ ID NO: 14 is the determined 3' cDNA sequence for J1-13

SEQ ID NO: 15 is the determined 5' cDNA sequence for J1-13

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SEQ ID NO: 50 is the determined cDNA sequence for P38

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SEQ ID NO: 108 is the predicted amino acid sequence for F1-12
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SEQ ID NO: 239 is the determined cDNA sequence for JPTPN39
SEQ ID NO: 240 is the determined cDNA sequence for JPTPN40
SEQ ID NO: 241 is the determined cDNA sequence for JPTPN41
SEQ ID NO: 242 is the determined cDNA sequence for JPTPN42
SEQ ID NO: 243 is the determined cDNA sequence for JPTPN45
SEQ ID NO: 244 is the determined cDNA sequence for JPTPN46
SEQ ID NO: 245 is the determined cDNA sequence for JPTPN51
SEQ ID NO: 246 is the determined cDNA sequence for JPTPN56
SEQ ID NO: 247 is the determined cDNA sequence for PTPN64
SEQ ID NO: 248 is the determined cDNA sequence for JPTPN65
SEQ ID NO: 249 is the determined cDNA sequence for JPTPN67
SEQ ID NO: 250 is the determined cDNA sequence for JPTPN76
SEQ ID NO: 251 is the determined cDNA sequence for JPTPN84
SEQ ID NO: 252 is the determined cDNA sequence for JPTPN85
SEQ ID NO: 253 is the determined cDNA sequence for JPTPN86
SEQ ID NO: 254 is the determined cDNA sequence for JPTPN87
SEQ ID NO: 255 is the determined cDNA sequence for JPTPN88
SEQ ID NO: 256 is the determined cDNA sequence for JP1F1
SEQ ID NO: 257 is the determined cDNA sequence for JP1F2
SEQ ID NO: 258 is the determined cDNA sequence for JP1C2

SEQ ID NO: 259 is the determined cDNA sequence for JP1B1
SEQ ID NO: 260 is the determined cDNA sequence for JP1B2
SEQ ID NO: 261 is the determined cDNA sequence for JP1D3
SEQ ID NO: 262 is the determined cDNA sequence for JP1A4
SEQ ID NO: 263 is the determined cDNA sequence for JP1F5
SEQ ID NO: 264 is the determined cDNA sequence for JP1E6
SEQ ID NO: 265 is the determined cDNA sequence for JP1D6
SEQ ID NO: 266 is the determined cDNA sequence for JP1B5
SEQ ID NO: 267 is the determined cDNA sequence for JP1A6
SEQ ID NO: 268 is the determined cDNA sequence for JP1E8
SEQ ID NO: 269 is the determined cDNA sequence for JP1D7
SEQ ID NO: 270 is the determined cDNA sequence for JP1D9
SEQ ID NO: 271 is the determined cDNA sequence for JP1C10
SEQ ID NO: 272 is the determined cDNA sequence for JP1A9
SEQ ID NO: 273 is the determined cDNA sequence for JP1F12
SEQ ID NO: 274 is the determined cDNA sequence for JP1E12
SEQ ID NO: 275 is the determined cDNA sequence for JP1D11
SEQ ID NO: 276 is the determined cDNA sequence for JP1C11
SEQ ID NO: 277 is the determined cDNA sequence for JP1C12
SEQ ID NO: 278 is the determined cDNA sequence for JP1B12
SEQ ID NO: 279 is the determined cDNA sequence for JP1A12
SEQ ID NO: 280 is the determined cDNA sequence for JP8G2
SEQ ID NO: 281 is the determined cDNA sequence for JP8H1
SEQ ID NO: 282 is the determined cDNA sequence for JP8H2
SEQ ID NO: 283 is the determined cDNA sequence for JP8A3
SEQ ID NO: 284 is the determined cDNA sequence for JP8A4
SEQ ID NO: 285 is the determined cDNA sequence for JP8C3
SEQ ID NO: 286 is the determined cDNA sequence for JP8G4
SEQ ID NO: 287 is the determined cDNA sequence for JP8B6
SEQ ID NO: 288 is the determined cDNA sequence for JP8D6

SEQ ID NO: 289 is the determined cDNA sequence for JP8F5
SEQ ID NO: 290 is the determined cDNA sequence for JP8A8
SEQ ID NO: 291 is the determined cDNA sequence for JP8C7
SEQ ID NO: 292 is the determined cDNA sequence for JP8D7
SEQ ID NO: 293 is the determined cDNA sequence for P8D8
SEQ ID NO: 294 is the determined cDNA sequence for JP8E7
SEQ ID NO: 295 is the determined cDNA sequence for JP8F8
SEQ ID NO: 296 is the determined cDNA sequence for JP8G8
SEQ ID NO: 297 is the determined cDNA sequence for JP8B10
SEQ ID NO: 298 is the determined cDNA sequence for JP8C10
SEQ ID NO: 299 is the determined cDNA sequence for JP8E9
SEQ ID NO: 300 is the determined cDNA sequence for JP8E10
SEQ ID NO: 301 is the determined cDNA sequence for JP8F9
SEQ ID NO: 302 is the determined cDNA sequence for JP8H9
SEQ ID NO: 303 is the determined cDNA sequence for JP8C12
SEQ ID NO: 304 is the determined cDNA sequence for JP8E11
SEQ ID NO: 305 is the determined cDNA sequence for JP8E12
SEQ ID NO: 306 is the amino acid sequence for the peptide PS2#12
SEQ ID NO: 307 is the determined cDNA sequence for P711P
SEQ ID NO: 308 is the determined cDNA sequence for P712P
SEQ ID NO: 309 is the determined cDNA sequence for CLONE23
SEQ ID NO: 310 is the determined cDNA sequence for P774P
SEQ ID NO: 311 is the determined cDNA sequence for P775P
SEQ ID NO: 312 is the determined cDNA sequence for P715P
SEQ ID NO: 313 is the determined cDNA sequence for P710P
SEQ ID NO: 314 is the determined cDNA sequence for P767P
SEQ ID NO: 315 is the determined cDNA sequence for P768P
SEQ ID NO: 316-325 are the determined cDNA sequences of previously isolated genes
SEQ ID NO: 326 is the determined cDNA sequence for P703PDE5
SEQ ID NO: 327 is the predicted amino acid sequence for P703PDE5

SEQ ID NO: 328 is the determined cDNA sequence for P703P6.26

SEQ ID NO: 329 is the predicted amino acid sequence for P703P6.26

SEQ ID NO: 330 is the determined cDNA sequence for P703PX-23

SEQ ID NO: 331 is the predicted amino acid sequence for P703PX-23

SEQ ID NO: 332 is the determined full length cDNA sequence for P509S

SEQ ID NO: 333 is the determined extended cDNA sequence for P707P (also referred to as 11-C9)

SEQ ID NO: 334 is the determined cDNA sequence for P714P

SEQ ID NO: 335 is the determined cDNA sequence for P705P (also referred to as 9-F3)

SEQ ID NO: 336 is the predicted amino acid sequence for P705P

SEQ ID NO: 337 is the amino acid sequence of the peptide P1S#10

SEQ ID NO: 338 is the amino acid sequence of the peptide p5

SEQ ID NO: 339 is the predicted amino acid sequence of P509S

SEQ ID NO: 340 is the determined cDNA sequence for P778P

SEQ ID NO: 341 is the determined cDNA sequence for P786P

SEQ ID NO: 342 is the determined cDNA sequence for P789P

SEQ ID NO: 343 is the determined cDNA sequence for a clone showing homology to Homo sapiens MM46 mRNA

SEQ ID NO: 344 is the determined cDNA sequence for a clone showing homology to Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA

SEQ ID NO: 345 is the determined cDNA sequence for a clone showing homology to Homo sapiens mRNA for E-cadherin

SEQ ID NO: 346 is the determined cDNA sequence for a clone showing homology to Human nuclear-encoded mitochondrial serine hydroxymethyltransferase (SHMT)

SEQ ID NO: 347 is the determined cDNA sequence for a clone showing homology to Homo sapiens natural resistance-associated macrophage protein2 (NRAMP2)

SEQ ID NO: 348 is the determined cDNA sequence for a clone showing homology to Homo sapiens phosphoglucomutase-related protein (PGMRP)

SEQ ID NO: 349 is the determined cDNA sequence for a clone showing homology to Human mRNA for proteosome subunit p40

SEQ ID NO: 350 is the determined cDNA sequence for P777P

SEQ ID NO: 351 is the determined cDNA sequence for P779P

SEQ ID NO: 352 is the determined cDNA sequence for P790P

SEQ ID NO: 353 is the determined cDNA sequence for P784P

SEQ ID NO: 354 is the determined cDNA sequence for P776P

SEQ ID NO: 355 is the determined cDNA sequence for P780P

SEQ ID NO: 356 is the determined cDNA sequence for P544S

SEQ ID NO: 357 is the determined cDNA sequence for P745S

SEQ ID NO: 358 is the determined cDNA sequence for P782P

SEQ ID NO: 359 is the determined cDNA sequence for P783P

SEQ ID NO: 360 is the determined cDNA sequence for unknown 17984

SEQ ID NO: 361 is the determined cDNA sequence for P787P

SEQ ID NO: 362 is the determined cDNA sequence for P788P

SEQ ID NO: 363 is the determined cDNA sequence for unknown 17994

SEQ ID NO: 364 is the determined cDNA sequence for P781P

SEQ ID NO: 365 is the determined cDNA sequence for P785P

SEQ ID NO: 366-375 are the determined cDNA sequences for splice variants of B305D.

SEQ ID NO: 376 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 366.

SEQ ID NO: 377 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 372.

SEQ ID NO: 378 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 373.

SEQ ID NO: 379 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 374.

SEQ ID NO: 380 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 375.

SEQ ID NO: 381 is the determined cDNA sequence for B716P.
SEQ ID NO: 382 is the determined full-length cDNA sequence for P711P.
SEQ ID NO: 383 is the predicted amino acid sequence for P711P.
SEQ ID NO: 384 is the cDNA sequence for P1000C.
SEQ ID NO: 385 is the cDNA sequence for CGI-82.
SEQ ID NO: 386 is the cDNA sequence for 23320.
SEQ ID NO: 387 is the cDNA sequence for CGI-69.
SEQ ID NO: 388 is the cDNA sequence for L-iditol-2-dehydrogenase.
SEQ ID NO: 389 is the cDNA sequence for 23379.
SEQ ID NO: 390 is the cDNA sequence for 23381.
SEQ ID NO: 391 is the cDNA sequence for KIAA0122.
SEQ ID NO: 392 is the cDNA sequence for 23399.
SEQ ID NO: 393 is the cDNA sequence for a previously identified gene.
SEQ ID NO: 394 is the cDNA sequence for HCLBP.
SEQ ID NO: 395 is the cDNA sequence for transglutaminase.
SEQ ID NO: 396 is the cDNA sequence for a previously identified gene.
SEQ ID NO: 397 is the cDNA sequence for PAP.
SEQ ID NO: 398 is the cDNA sequence for Ets transcription factor PDEF.
SEQ ID NO: 399 is the cDNA sequence for hTGR.
SEQ ID NO: 400 is the cDNA sequence for KIAA0295.
SEQ ID NO: 401 is the cDNA sequence for 22545.
SEQ ID NO: 402 is the cDNA sequence for 22547.
SEQ ID NO: 403 is the cDNA sequence for 22548.
SEQ ID NO: 404 is the cDNA sequence for 22550.
SEQ ID NO: 405 is the cDNA sequence for 22551.
SEQ ID NO: 406 is the cDNA sequence for 22552.
SEQ ID NO: 407 is the cDNA sequence for 22553.
SEQ ID NO: 408 is the cDNA sequence for 22558.
SEQ ID NO: 409 is the cDNA sequence for 22562.
SEQ ID NO: 410 is the cDNA sequence for 22565.

SEQ ID NO:411 is the cDNA sequence for 22567.
SEQ ID NO:412 is the cDNA sequence for 22568.
SEQ ID NO:413 is the cDNA sequence for 22570.
SEQ ID NO:414 is the cDNA sequence for 22571.
SEQ ID NO:415 is the cDNA sequence for 22572.
SEQ ID NO:416 is the cDNA sequence for 22573.
SEQ ID NO:417 is the cDNA sequence for 22573.
SEQ ID NO:418 is the cDNA sequence for 22575.
SEQ ID NO:419 is the cDNA sequence for 22580.
SEQ ID NO:420 is the cDNA sequence for 22581.
SEQ ID NO:421 is the cDNA sequence for 22582.
SEQ ID NO:422 is the cDNA sequence for 22583.
SEQ ID NO:423 is the cDNA sequence for 22584.
SEQ ID NO:424 is the cDNA sequence for 22585.
SEQ ID NO:425 is the cDNA sequence for 22586.
SEQ ID NO:426 is the cDNA sequence for 22587.
SEQ ID NO:427 is the cDNA sequence for 22588.
SEQ ID NO:428 is the cDNA sequence for 22589.
SEQ ID NO:429 is the cDNA sequence for 22590.
SEQ ID NO:430 is the cDNA sequence for 22591.
SEQ ID NO:431 is the cDNA sequence for 22592.
SEQ ID NO:432 is the cDNA sequence for 22593.
SEQ ID NO:433 is the cDNA sequence for 22594.
SEQ ID NO:434 is the cDNA sequence for 22595.
SEQ ID NO:435 is the cDNA sequence for 22596.
SEQ ID NO:436 is the cDNA sequence for 22847.
SEQ ID NO:437 is the cDNA sequence for 22848.
SEQ ID NO:438 is the cDNA sequence for 22849.
SEQ ID NO:439 is the cDNA sequence for 22851.
SEQ ID NO:440 is the cDNA sequence for 22852.

SEQ ID NO:441 is the cDNA sequence for 22853.
SEQ ID NO:442 is the cDNA sequence for 22854.
SEQ ID NO:443 is the cDNA sequence for 22855.
SEQ ID NO:444 is the cDNA sequence for 22856.
SEQ ID NO:445 is the cDNA sequence for 22857.
SEQ ID NO:446 is the cDNA sequence for 23601.
SEQ ID NO:447 is the cDNA sequence for 23602.
SEQ ID NO:448 is the cDNA sequence for 23605.
SEQ ID NO:449 is the cDNA sequence for 23606.
SEQ ID NO:450 is the cDNA sequence for 23612.
SEQ ID NO:451 is the cDNA sequence for 23614.
SEQ ID NO:452 is the cDNA sequence for 23618.
SEQ ID NO:453 is the cDNA sequence for 23622.
SEQ ID NO:454 is the cDNA sequence for folate hydrolase.
SEQ ID NO:455 is the cDNA sequence for LIM protein.
SEQ ID NO:456 is the cDNA sequence for a known gene.
SEQ ID NO:457 is the cDNA sequence for a known gene.
SEQ ID NO:458 is the cDNA sequence for a previously identified gene.
SEQ ID NO:459 is the cDNA sequence for 23045.
SEQ ID NO:460 is the cDNA sequence for 23032.
SEQ ID NO:461 is the cDNA sequence for 23054.
SEQ ID NOs:462-467 are cDNA sequences for known genes.
SEQ ID NOs:468-471 are cDNA sequences for P710P.
SEQ ID NO:472 is a cDNA sequence for P1001C.
SEQ ID NO:473 is the amino acid sequence for PSMA.
SEQ ID NO:474 is the amino acid sequence for PAP.
SEQ ID NO:475 is the amino acid sequence for PSA.
SEQ ID NO:476 is the amino acid sequence for a fusion protein containing PSA, P703P and P501S.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the therapy and diagnosis of cancer, such as prostate cancer. The compositions described herein may include prostate tumor polypeptides, polynucleotides encoding such polypeptides, binding agents such as antibodies, antigen presenting cells (APCs) and/or immune system cells (*e.g.*, T cells). Polypeptides of the present invention generally comprise at least a portion (such as an immunogenic portion) of a prostate tumor protein or a variant thereof. A "prostate tumor protein" is a protein that is expressed in prostate tumor cells at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in a normal tissue, as determined using a representative assay provided herein. Certain prostate tumor proteins are tumor proteins that react detectably (within an immunoassay, such as an ELISA or Western blot) with antisera of a patient afflicted with prostate cancer. Polynucleotides of the subject invention generally comprise a DNA or RNA sequence that encodes all or a portion of such a polypeptide, or that is complementary to such a sequence. Antibodies are generally immune system proteins, or antigen-binding fragments thereof, that are capable of binding to a polypeptide as described above. Antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B-cells that express a polypeptide as described above. T cells that may be employed within such compositions are generally T cells that are specific for a polypeptide as described above.

The present invention is based on the discovery of human prostate tumor proteins. Sequences of polynucleotides encoding certain tumor proteins, or portions thereof, are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Sequences of polypeptides comprising at least a portion of a tumor protein are provided in SEQ ID NOs:112-114, 172, 176, 178, 327, 329, 331, 336, 339, 376-380 and 383.

PROSTATE TUMOR PROTEIN POLYNUCLEOTIDES

Any polynucleotide that encodes a prostate tumor protein or a portion or other variant thereof as described herein is encompassed by the present invention. Preferred polynucleotides comprise at least 15 consecutive nucleotides, preferably at least 30 consecutive nucleotides and more preferably at least 45 consecutive nucleotides, that encode a portion of a prostate tumor protein. More preferably, a polynucleotide encodes an immunogenic portion of a prostate tumor protein. Polynucleotides complementary to any such sequences are also encompassed by the present invention. Polynucleotides may be single-stranded (coding or antisense) or double-stranded, and may be DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a prostate tumor protein or a portion thereof) or may comprise a variant of such a sequence. Polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the immunogenicity of the encoded polypeptide is not diminished, relative to a native tumor protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native prostate tumor protein or a portion thereof.

Two polynucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acids in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions,

usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the “percentage of sequence identity” is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Variants may also, or alternatively, be substantially homologous to a native gene, or a portion or complement thereof. Such polynucleotide variants are

capable of hybridizing under moderately stringent conditions to a naturally occurring DNA sequence encoding a native prostate tumor protein (or a complementary sequence). Suitable moderately stringent conditions include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not, have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Polynucleotides may be prepared using any of a variety of techniques. For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least five fold greater in a prostate tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as prostate tumor cells. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a prostate tumor cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with ^{32}P) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using, for example, software well known in the art. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids Res.* 19:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence.

Certain nucleic acid sequences of cDNA molecules encoding at least a portion of a prostate tumor protein are provided in SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472. Isolation of these polynucleotides is described below. Each of these prostate tumor proteins was overexpressed in prostate tumor tissue.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may

also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a prostate tumor protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a prostate tumor polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a tumor protein. Antisense technology can be used to control gene expression through triple-helix formation, which compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (*see* Gee et al., *In* Huber and Carr, *Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (*e.g.*, promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Within certain embodiments, polynucleotides may be formulated so as to permit entry into a cell of a mammal, and expression therein. Such formulations are particularly useful for therapeutic purposes, as described below. Those of ordinary skill in the art will appreciate that there are many ways to achieve expression of a polynucleotide in a target cell, and any suitable method may be employed. For example, a polynucleotide may be incorporated into a viral vector such as, but not limited to, adenovirus, adeno-associated virus, retrovirus, or vaccinia or other pox virus (*e.g.*, avian pox virus). Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The preparation and use of such systems is well known in the art.

PROSTATE TUMOR POLYPEPTIDES

Within the context of the present invention, polypeptides may comprise at least an immunogenic portion of a prostate tumor protein or a variant thereof, as described herein. As noted above, a "prostate tumor protein" is a protein that is expressed by prostate tumor cells. Proteins that are prostate tumor proteins also react detectably within an immunoassay (such as an ELISA) with antisera from a patient with prostate cancer. Polypeptides as described herein may be of any length. Additional sequences derived from the native protein and/or heterologous sequences may be present, and such sequences may (but need not) possess further immunogenic or antigenic properties.

An "immunogenic portion," as used herein is a portion of a protein that is recognized (*i.e.*, specifically bound) by a B-cell and/or T-cell surface antigen receptor. Such immunogenic portions generally comprise at least 5 amino acid residues, more preferably at least 10, and still more preferably at least 20 amino acid residues of a prostate tumor protein or a variant thereof. Certain preferred immunogenic portions include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other preferred immunogenic portions may contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids), relative to the mature protein.

Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera

and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native prostate tumor protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A.

As noted above, a composition may comprise a variant of a native prostate tumor protein. A polypeptide "variant," as used herein, is a polypeptide that differs from a native prostate tumor protein in one or more substitutions, deletions, additions and/or insertions, such that the immunogenicity of the polypeptide is not substantially diminished. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most

preferably at least about 95% identity (determined as described above) to the identified polypeptides.

Preferably, a variant contains conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (*e.g.*, poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

Polypeptides may be prepared using any of a variety of well known techniques. Recombinant polypeptides encoded by DNA sequences as described above may be readily prepared from the DNA sequences using any of a variety of expression

vectors known to those of ordinary skill in the art. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. Supernatants from suitable host/vector systems which secrete recombinant protein or polypeptide into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant polypeptide.

Portions and other variants having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may also be generated by synthetic means, using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be

targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein.

In certain embodiments, the present invention provides fusion proteins comprising a polypeptide disclosed herein together with at least one of the following known prostate antigens: prostate specific antigen (PSA); prostatic acid phosphatase (PAP); and prostate specific membrane antigen (PSMA). The protein sequences for PSMA, PAP and PSA are provided in SEQ ID NO: 473-475, respectively. In certain embodiments, the fusion proteins of the present invention comprise PSA, PAP and/or PSMA in combination with one or more of the following the inventive antigens: P501S (amino acid sequence provided in SEQ ID NO: 113); P703P (amino acid sequences provided in SEQ ID NO: 327, 329, 331); P704P (cDNA sequence provided in SEQ ID NO: 67); P712P (cDNA sequence provided in SEQ ID NO: 308); P775P (cDNA sequence provided in SEQ ID NO: 311); P776P (cDNA sequence provided in SEQ ID NO: 354); P790P (cDNA sequence provided in SEQ ID NO: 352). The amino acid sequence of a fusion protein of PSA, P703P and P501S is provided in SEQ ID NO: 476. In preferred embodiments, the inventive fusion proteins comprise one of the following combinations of antigens: PSA and P703P; PSA and P501S; PAP and P703P; PAP and P501S; PSMA and P703P; PSMA and P501S; PSA, PAP and P703P; PSA, PAP and P501S; PSA, PAP, PSMA and P703P, PSA, PAP, PSMA and P501S. One of skill in the art will appreciate that the order of polypeptides within a fusion protein can be altered without substantially changing the therapeutic, prophylactic or diagnostic properties of the fusion protein.

The fusion proteins described above are more immunogenic and will be effective in a greater number of prostate cancer patients than any of the individual components alone. The use of multiple antigens in the form of a fusion protein also lessens the likelihood of immunologic escape.

Fusion proteins may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion protein is expressed as a recombinant protein, allowing the production of increased levels, relative to a non-fused protein, in an expression system. Briefly, DNA sequences encoding the polypeptide

components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion protein that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see*, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-

terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

In general, polypeptides (including fusion proteins) and polynucleotides as described herein are isolated. An "isolated" polypeptide or polynucleotide is one that is removed from its original environment. For example, a naturally-occurring protein is isolated if it is separated from some or all of the coexisting materials in the natural system. Preferably, such polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. A polynucleotide is considered to be isolated if, for example, it is cloned into a vector that is not a part of the natural environment.

BINDING AGENTS

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a prostate tumor protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a prostate tumor protein if it reacts at a detectable level (within, for example, an ELISA) with a prostate tumor protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a cancer, such as prostate cancer, using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a prostate tumor protein will generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, and will generate a negative signal

indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g.*, mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested

by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

T CELLS

Immunotherapeutic compositions may also, or alternatively, comprise T cells specific for a prostate tumor protein. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the CEPRATE™ system, available from CellPro Inc., Bothell WA (*see also* U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a prostate tumor polypeptide, polynucleotide encoding a prostate tumor polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the generation of T cells that are specific for the polypeptide. Preferably, a prostate tumor polypeptide or polynucleotide is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a prostate tumor polypeptide if the T cells kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively,

detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (*e.g.*, by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a prostate tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days should result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (*e.g.*, TNF or IFN-γ) is indicative of T cell activation (*see* Coligan et al., Current Protocols in Immunology, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a prostate tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4⁺ and/or CD8⁺. Prostate tumor protein-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from either a patient or a related, or unrelated, donor and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4⁺ or CD8⁺ T cells that proliferate in response to a prostate tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a prostate tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator cells that synthesize a prostate tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of a prostate tumor protein can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

PHARMACEUTICAL COMPOSITIONS AND VACCINES

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions

or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and a non-specific immune response enhancer. A non-specific immune response enhancer may be any substance that enhances an immune response to an exogenous antigen. Examples of non-specific immune response enhancers include adjuvants, biodegradable microspheres (*e.g.*, polylactic galactide) and liposomes (into which the compound is incorporated; *see e.g.*, Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other tumor antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner

et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be

formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, the adjuvant composition is preferably designed to induce an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (*e.g.*, IFN- γ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (*e.g.*, IL-4, IL-5, IL-6, IL-10 and TNF- β) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt.

MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT; see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule or sponge that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific

immune response that targets tumor cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*) and based on the lack of differentiation markers of B cells (CD19 and CD20), T cells (CD3), monocytes (CD14) and natural killer cells (CD56), as determined using standard assays. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF α to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into

dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF α , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc γ receptor, mannose receptor and DEC-205 marker. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80 and CD86).

APCs may generally be transfected with a polynucleotide encoding a prostate tumor protein (or portion or other variant thereof) such that the prostate tumor polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the prostate tumor polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be

pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

CANCER THERAPY

In further aspects of the present invention, the compositions described herein may be used for immunotherapy of cancer, such as prostate cancer. Within such methods, pharmaceutical compositions and vaccines are typically administered to a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions and vaccines may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. A cancer may be diagnosed using criteria generally accepted in the art, including the presence of a malignant tumor. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides disclosed herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8⁺ cytotoxic T lymphocytes and CD4⁺ T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The

polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see*, for example, Cheever et al., *Immunological Reviews* 157:177, 1997).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions disclosed herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous,

intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 100 μ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a prostate tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

METHODS FOR DETECTING CANCER

In general, a cancer may be detected in a patient based on the presence of one or more prostate tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, urine and/or tumor biopsies) obtained from

the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as prostate cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a prostate tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. *See, e.g.,* Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G, protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length prostate tumor proteins and portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 μ g, and preferably about 100 ng to about 1 μ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized

on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed

and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 μ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use prostate tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such prostate tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a prostate tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4⁺ and/or CD8⁺ T cells isolated from a patient is incubated with a prostate tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with prostate tumor polypeptide (*e.g.*, 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of prostate tumor polypeptide to serve as a control. For CD4⁺ T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8⁺ T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a prostate tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a prostate tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the prostate tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a prostate tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%,

preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a prostate tumor protein that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes will hybridize to a polynucleotide encoding a polypeptide disclosed herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence recited in SEQ ID NO: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375 and 381. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered positive.

In another embodiment, the disclosed compositions may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter

performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple prostate tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

DIAGNOSTIC KITS

The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a prostate tumor protein. Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

Alternatively, a kit may be designed to detect the level of mRNA encoding a prostate tumor protein in a biological sample. Such kits generally comprise

at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a prostate tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a prostate tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones

having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and SfuI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E.*

coli DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (referred to as "prostate subtraction 1").

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 μ g each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the

driver DNA and subtraction was performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114. L1-12 is also referred to as P501S.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (referred to as "prostate subtraction 2"). The determined cDNA sequences for these clones, hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (referred to as "prostate subtraction spike 2") was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193,

respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

Additional studies with prostate subtraction spike 2 resulted in the isolation of three more clones. Their sequences were determined as described above and compared to the most recent GenBank. All three clones were found to have homology to known genes, which are Cysteine-rich protein, KIAA0242, and KIAA0280 (SEQ ID NO: 317, 319, and 320, respectively). Further analysis of these clones by Synteni microarray (Synteni, Palo Alto, CA) demonstrated that all three clones were over-expressed in most prostate tumors and prostate BPH, as well as in the majority of normal prostate tissues tested, but low expression in all other normal tissues.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (referred to as "prostate subtraction 3"). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS: 93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA⁺ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively.

cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Additional, studies led to the isolation of the full-length cDNA sequence for P509S. This sequence is provided in SEQ ID NO: 332, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 339.

EXAMPLE 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17 (also referred to as P502S), L1-12 (also referred to as P501S), F1-12 (also referred to as P504S) and N1-1862 (also referred to as P503S) were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 μ g of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β -actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β -actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β -actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β -actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 (P502S) and L1-12 (P501S) appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 (P503S) was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17 (P502S), N1-1862 (P503S) and L1-12 (P501S) are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 (P504S) is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 (P501S) is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 (P502S) was detected in two prostate tumors and not in the other tissues tested. N1-1862 (P503S) was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 (P504S) was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The microarray technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 (P501S) was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 (P504S) were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 (P503S) was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-

expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Further microarray analysis to specifically address the extent to which P501S (SEQ ID NO: 110) was expressed in breast tumor revealed moderate over-expression not only in breast tumor, but also in metastatic breast tumor (2/31), with negligible to low expression in normal tissues. This data suggests that P501S may be over-expressed in various breast tumors as well as in prostate tumors.

The expression levels of 32 ESTs (expressed sequence tags) described by Vasmatazis *et al.* (*Proc. Natl. Acad. Sci. USA* 95:300-304, 1998) in a variety of tumor and normal tissues were examined by microarray technology as described above. Two of these clones (referred to as P1000C and P1001C) were found to be over-expressed in prostate tumor and normal prostate, and expressed at low to undetectable levels in all other tissues tested (normal aorta, thymus, resting and activated PBMC, epithelial cells, spinal cord, adrenal gland, fetal tissues, skin, salivary gland, large intestine, bone marrow, liver, lung, dendritic cells, stomach, lymph nodes, brain, heart, small intestine, skeletal muscle, colon and kidney. The determined cDNA sequences for P1000C and P1001C are provided in SEQ ID NO: 384 and 472, respectively. The sequence of P1001C was found to show some homology to the previously isolated Human mRNA for JM27 protein. No significant homologies were found to the sequence of P1000C.

The expression of the polypeptide encoded by the full length cDNA sequence for F1-12 (also referred to as P504S; SEQ ID NO: 108) was investigated by immunohistochemical analysis. Rabbit-anti-P504S polyclonal antibodies were generated against the full length P504S protein by standard techniques. Subsequent isolation and characterization of the polyclonal antibodies were also performed by techniques well known in the art. Immunohistochemical analysis showed that the P504S polypeptide was expressed in 100% of prostate carcinoma samples tested (n=5).

The rabbit-anti-P504S polyclonal antibody did not appear to label benign prostate cells with the same cytoplasmic granular staining, but rather with light nuclear staining. Analysis of normal tissues revealed that the encoded polypeptide was found to be expressed in some, but not all normal human tissues. Positive

cytoplasmic staining with rabbit-anti-P504S polyclonal antibody was found in normal human kidney, liver, brain, colon and lung-associated macrophages, whereas heart and bone marrow were negative.

This data indicates that the P504S polypeptide is present in prostate cancer tissues, and that there are qualitative and quantitative differences in the staining between benign prostatic hyperplasia tissues and prostate cancer tissues, suggesting that this polypeptide may be detected selectively in prostate tumors and therefore be useful in the diagnosis of prostate cancer.

EXAMPLE 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO: 41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO: 46, 53 and 66-68, respectively) were found to show some degree of homology to

previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. Larger cDNA clones containing the P20 sequence represent splice variants of a gene referred to as P703P. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The determined cDNA sequence for an extended spliced form of P703 is provided in SEQ ID NO: 225. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCR as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20, a portion of the P703P gene, was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor

compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, 9-f12 and 9-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, 9-f12 and 9-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequence of 9-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and 9-f12 were found to show some homology to previously identified genes. Further characterization of 7-G6 and 8-G3 showed identity to the known genes PAP and PSA, respectively.

mRNA expression levels for these clones were determined using the micro-array technology described above. The clones 7-G6, 8-G3, 8-B5, 8-B6, 8-D4, 8-D9, 9-F3, 9-F12, 9-H3, 10-A2, 10-A4, 11-C9 and 11-F2 were found to be over-expressed in prostate tumor and normal prostate, with expression in other tissues tested being low or undetectable. Increased expression of 8-F11 was seen in prostate tumor

and normal prostate, bladder, skeletal muscle and colon. Increased expression of 10-H10 was seen in prostate tumor and normal prostate, bladder, lung, colon, brain and large intestine. Increased expression of 9-B1 was seen in prostate tumor, breast tumor, and normal prostate, salivary gland, large intestine and skin, with increased expression of 11-C8 being seen in prostate tumor, and normal prostate and large intestine.

An additional cDNA fragment derived from the PCR-based normal prostate subtraction, described above, was found to be prostate specific by both microarray technology and RT-PCR. The determined cDNA sequence of this clone (referred to as 9-A11) is provided in SEQ ID NO: 226. Comparison of this sequence with those in the public databases revealed 99% identity to the known gene HOXB13.

Further studies led to the isolation of the clones 8-C6 and 8-H7. The determined cDNA sequences for these clones are provided in SEQ ID NO: 227 and 228, respectively. These sequences were found to show some homology to previously isolated ESTs.

PCR and hybridization-based methodologies were employed to obtain longer cDNA sequences for clone P20 (also referred to as P703P), yielding three additional cDNA fragments that progressively extend the 5' end of the gene. These fragments, referred to as P703PDE5, P703P6.26, and P703PX-23 (SEQ ID NO: 326, 328 and 330, with the predicted corresponding amino acid sequences being provided in SEQ ID NO: 327, 329 and 331, respectively) contain additional 5' sequence. P703PDE5 was recovered by screening of a cDNA library (#141-26) with a portion of P703P as a probe. P703P6.26 was recovered from a mixture of three prostate tumor cDNAs and P703PX_23 was recovered from cDNA library (#438-48). Together, the additional sequences include all of the putative mature serine protease along with part of the putative signal sequence. Further studies using a PCR-based subtraction library of a prostate tumor pool subtracted against a pool of normal tissues (referred to as JP: PCR subtraction) resulted in the isolation of thirteen additional clones, seven of which did not share any significant homology to known GenBank sequences. The determined cDNA sequences for these seven clones (P711P, P712P, novel 23, P774P, P775P, P710P and P768P) are provided in SEQ ID NO: 307-311, 313 and 315, respectively.

The remaining six clones (SEQ ID NO: 316 and 321-325) were shown to share some homology to known genes. By microarray analysis, all thirteen clones showed three or more fold over-expression in prostate tissues, including prostate tumors, BPH and normal prostate as compared to normal non-prostate tissues. Clones P711P, P712P, novel 23 and P768P showed over-expression in most prostate tumors and BPH tissues tested (n=29), and in the majority of normal prostate tissues (n=4), but background to low expression levels in all normal tissues. Clones P774P, P775P and P710P showed comparatively lower expression and expression in fewer prostate tumors and BPH samples, with negative to low expression in normal prostate.

The full-length cDNA for P711P was obtained by employing the partial sequence of SEQ ID NO: 307 to screen a prostate cDNA library. Specifically, a directionally cloned prostate cDNA library was prepared using standard techniques. One million colonies of this library were plated onto LB/Amp plates. Nylon membrane filters were used to lift these colonies, and the cDNAs which were picked up by these filters were denatured and cross-linked to the filters by UV light. The P711P cDNA fragment of SEQ ID NO: 307 was radio-labeled and used to hybridize with these filters. Positive clones were selected, and cDNAs were prepared and sequenced using an automatic Perkin Elmer/Applied Biosystems sequencer. The determined full-length sequence of P711P is provided in SEQ ID NO: 382, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 383.

Using PCR and hybridization-based methodologies, additional cDNA sequence information was derived for two clones described above, 11-C9 and 9-F3, herein after referred to as P707P and P714P, respectively (SEQ ID NO: 333 and 334). After comparison with the most recent GenBank, P707P was found to be a splice variant of the known gene HoxB13. In contrast, no significant homologies to P714P were found.

Clones 8-B3, P89, P98, P130 and P201 (as disclosed in U.S. Patent Application No. 09/020,956, filed February 9, 1998) were found to be contained within one contiguous sequence, referred to as P705P (SEQ ID NO: 335, with the predicted

amino acid sequence provided in SEQ ID NO: 336), which was determined to be a splice variant of the known gene NKX 3.1.

EXAMPLE 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

EXAMPLE 5

FURTHER ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA library generated from prostate primary tumor mRNA as described above was subtracted with cDNA from normal prostate. The subtraction was performed using a PCR-based protocol (Clontech), which was modified to generate larger fragments. Within this protocol, tester and driver double stranded cDNA were

separately digested with five restriction enzymes that recognize six-nucleotide restriction sites (MluI, MscI, PvuII, SalI and StuI). This digestion resulted in an average cDNA size of 600 bp, rather than the average size of 300 bp that results from digestion with RsaI according to the Clontech protocol. This modification did not affect the subtraction efficiency. Two tester populations were then created with different adapters, and the driver library remained without adapters.

The tester and driver libraries were then hybridized using excess driver cDNA. In the first hybridization step, driver was separately hybridized with each of the two tester cDNA populations. This resulted in populations of (a) unhybridized tester cDNAs, (b) tester cDNAs hybridized to other tester cDNAs, (c) tester cDNAs hybridized to driver cDNAs and (d) unhybridized driver cDNAs. The two separate hybridization reactions were then combined, and rehybridized in the presence of additional denatured driver cDNA. Following this second hybridization, in addition to populations (a) through (d), a fifth population (e) was generated in which tester cDNA with one adapter hybridized to tester cDNA with the second adapter. Accordingly, the second hybridization step resulted in enrichment of differentially expressed sequences which could be used as templates for PCR amplification with adaptor-specific primers.

The ends were then filled in, and PCR amplification was performed using adaptor-specific primers. Only population (e), which contained tester cDNA that did not hybridize to driver cDNA, was amplified exponentially. A second PCR amplification step was then performed, to reduce background and further enrich differentially expressed sequences.

This PCR-based subtraction technique normalizes differentially expressed cDNAs so that rare transcripts that are overexpressed in prostate tumor tissue may be recoverable. Such transcripts would be difficult to recover by traditional subtraction methods.

In addition to genes known to be overexpressed in prostate tumor, seventy-seven further clones were identified. Sequences of these partial cDNAs are provided in SEQ ID NO: 29 to 305. Most of these clones had no significant homology to database sequences. Exceptions were JPTPN23 (SEQ ID NO: 231; similarity to pig

valosin-containing protein), JPTPN30 (SEQ ID NO: 234; similarity to rat mRNA for proteasome subunit), JPTPN45 (SEQ ID NO: 243; similarity to rat *norvegicus* cytosolic NADP-dependent isocitrate dehydrogenase), JPTPN46 (SEQ ID NO: 244; similarity to human subclone H8 4 d4 DNA sequence), JP1D6 (SEQ ID NO: 265; similarity to *G. gallus* dynein light chain-A), JP8D6 (SEQ ID NO: 288; similarity to human BAC clone RG016J04), JP8F5 (SEQ ID NO: 289; similarity to human subclone H8 3 b5 DNA sequence), and JP8E9 (SEQ ID NO: 299; similarity to human Alu sequence).

Additional studies using the PCR-based subtraction library consisting of a prostate tumor pool subtracted against a normal prostate pool (referred to as PT-PN PCR subtraction) yielded three additional clones. Comparison of the cDNA sequences of these clones with the most recent release of GenBank revealed no significant homologies to the two clones referred to as P715P and P767P (SEQ ID NO: 312 and 314). The remaining clone was found to show some homology to the known gene KIAA0056 (SEQ ID NO: 318). Using microarray analysis to measure mRNA expression levels in various tissues, all three clones were found to be over-expressed in prostate tumors and BPH tissues. Specifically, clone P715P was over-expressed in most prostate tumors and BPH tissues by a factor of three or greater, with elevated expression seen in the majority of normal prostate samples and in fetal tissue, but negative to low expression in all other normal tissues. Clone P767P was over-expressed in several prostate tumors and BPH tissues, with moderate expression levels in half of the normal prostate samples, and background to low expression in all other normal tissues tested.

Further analysis, by microarray as described above, of the PT-PN PCR subtraction library and of a DNA subtraction library containing cDNA from prostate tumor subtracted with a pool of normal tissue cDNAs, led to the isolation of 27 additional clones (SEQ ID NO: 340-365 and 381) which were determined to be over-expressed in prostate tumor. The clones of SEQ ID NO: 341, 342, 345, 347, 348, 349, 351, 355-359, 361, 362 and 364 were also found to be expressed in normal prostate. Expression of all 26 clones in a variety of normal tissues was found to be low or undetectable, with the exception of P544S (SEQ ID NO: 356) which was found to be

expressed in small intestine. Of the 26 clones, 10 (SEQ ID NO: 340-349) were found to show some homology to previously identified sequences. No significant homologies were found to the clones of SEQ ID NO: 350-365.

EXAMPLE 6

PEPTIDE PRIMING OF MICE AND PROPAGATION OF CTL LINES

6.1. This Example illustrates the preparation of a CTL cell line specific for cells expressing the P502S gene.

Mice expressing the transgene for human HLA A2.1 (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with P2S#12 peptide (VLGWVAEL; SEQ ID NO: 306), which is derived from the P502S gene (also referred to herein as J1-17, SEQ ID NO: 8), as described by Theobald et al., *Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995 with the following modifications. Mice were immunized with 100µg of P2S#12 and 120µg of an I-A^b binding peptide derived from hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and using a nylon mesh single cell suspensions prepared. Cells were then resuspended at 6×10^6 cells/ml in complete media (RPMI-1640; Gibco BRL, Gaithersburg, MD) containing 10% FCS, 2mM Glutamine (Gibco BRL), sodium pyruvate (Gibco BRL), non-essential amino acids (Gibco BRL), 2×10^{-5} M 2-mercaptoethanol, 50U/ml penicillin and streptomycin, and cultured in the presence of irradiated (3000 rads) P2S#12-pulsed (5mg/ml P2S#12 and 10mg/ml β2-microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of 7µg/ml dextran sulfate and 25µg/ml LPS for 3 days). Six days later, cells (5×10^5 /ml) were restimulated with 2.5×10^6 /ml peptide pulsed irradiated (20,000 rads) EL4A2Kb cells (Sherman et al, *Science* 258:815-818, 1992) and 3×10^6 /ml A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20U/ml IL-2. Cells continued to be restimulated on a weekly basis as described, in preparation for cloning the line.

P2S#12 line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells

as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, clones that were growing were isolated and maintained in culture. Several of these clones demonstrated significantly higher reactivity (lysis) against human fibroblasts (HLA A2.1 expressing) transduced with P502S than against control fibroblasts. An example is presented in Figure 1.

This data indicates that P2S #12 represents a naturally processed epitope of the P502S protein that is expressed in the context of the human HLA A2.1 molecule.

6.2. This Example illustrates the preparation of murine CTL lines and CTL clones specific for cells expressing the P501S gene.

This series of experiments were performed similarly to that described above. Mice were immunized with the P1S#10 peptide (SEQ ID NO: 337), which is derived from the P501S gene (also referred to herein as L1-12, SEQ ID NO: 110). The P1S#10 peptide was derived by analysis of the predicted polypeptide sequence for P501S for potential HLA-A2 binding sequences as defined by published HLA-A2 binding motifs (Parker, KC, *et al*, *J. Immunol.*, 152:163, 1994). P1S#10 peptide was synthesized as described in Example 4, and empirically tested for HLA-A2 binding using a T cell based competition assay. Predicted A2 binding peptides were tested for their ability to compete HLA-A2 specific peptide presentation to an HLA-A2 restricted CTL clone (D150M58), which is specific for the HLA-A2 binding influenza matrix peptide fluM58. D150M58 CTL secretes TNF in response to self-presentation of peptide fluM58. In the competition assay, test peptides at 100-200 $\mu\text{g/ml}$ were added to cultures of D150M58 CTL in order to bind HLA-A2 on the CTL. After thirty minutes, CTL cultured with test peptides, or control peptides, were tested for their antigen dose response to the fluM58 peptide in a standard TNF bioassay. As shown in Figure 3, peptide P1S#10 competes HLA-A2 restricted presentation of fluM58, demonstrating that peptide P1S#10 binds HLA-A2.

Mice expressing the transgene for human HLA A2.1 were immunized as described by Theobald et al. (*Proc. Natl. Acad. Sci. USA* 92:11993-11997, 1995) with the following modifications. Mice were immunized with 62.5 μg of P1S #10 and 120 μg

of an I-A^b binding peptide derived from Hepatitis B Virus protein emulsified in incomplete Freund's adjuvant. Three weeks later these mice were sacrificed and single cell suspensions prepared using a nylon mesh. Cells were then resuspended at 6×10^6 cells/ml in complete media (as described above) and cultured in the presence of irradiated (3000 rads) P1S#10-pulsed ($2\mu\text{g/ml}$ P1S#10 and 10mg/ml $\beta 2$ -microglobulin) LPS blasts (A2 transgenic spleens cells cultured in the presence of $7\mu\text{g/ml}$ dextran sulfate and $25\mu\text{g/ml}$ LPS for 3 days). Six days later cells ($5 \times 10^5/\text{ml}$) were restimulated with $2.5 \times 10^6/\text{ml}$ peptide-pulsed irradiated (20,000 rads) EL4A2Kb cells, as described above, and $3 \times 10^6/\text{ml}$ A2 transgenic spleen feeder cells. Cells were cultured in the presence of 20 U/ml IL-2. Cells were restimulated on a weekly basis in preparation for cloning. After three rounds of *in vitro* stimulations, one line was generated that recognized P1S#10-pulsed Jurkat A2Kb targets and P501S-transduced Jurkat targets as shown in Figure 4.

A P1S#10-specific CTL line was cloned by limiting dilution analysis with peptide pulsed EL4 A2Kb tumor cells (1×10^4 cells/ well) as stimulators and A2 transgenic spleen cells as feeders (5×10^5 cells/ well) grown in the presence of 30U/ml IL-2. On day 14, cells were restimulated as before. On day 21, viable clones were isolated and maintained in culture. As shown in Figure 5, five of these clones demonstrated specific cytolytic reactivity against P501S-transduced Jurkat A2Kb targets. This data indicates that P1S#10 represents a naturally processed epitope of the P501S protein that is expressed in the context of the human HLA-A2.1 molecule.

EXAMPLE 7

ABILITY OF HUMAN T CELLS TO RECOGNIZE PROSTATE TUMOR POLYPEPTIDES

This Example illustrates the ability of T cells specific for a prostate tumor polypeptide to recognize human tumor.

Human CD8⁺ T cells were primed *in vitro* to the P2S-12 peptide (SEQ ID NO: 306) derived from P502S (also referred to as J1-17) using dendritic cells according to the protocol of Van Tsai et al. (*Critical Reviews in Immunology* 18:65-75, 1998). The resulting CD8⁺ T cell microcultures were tested for their ability to recognize the P2S-12 peptide presented by autologous fibroblasts or fibroblasts which were transduced to express the P502S gene in a γ -interferon ELISPOT assay (*see* Lalvani et al., *J. Exp. Med.* 186:859-865, 1997). Briefly, titrating numbers of T cells were assayed in duplicate on 10⁴ fibroblasts in the presence of 3 μ g/ml human β_2 -microglobulin and 1 μ g/ml P2S-12 peptide or control E75 peptide. In addition, T cells were simultaneously assayed on autologous fibroblasts transduced with the P502S gene or as a control, fibroblasts transduced with HER-2/*neu*. Prior to the assay, the fibroblasts were treated with 10 ng/ml γ -interferon for 48 hours to upregulate class I MHC expression. One of the microcultures (#5) demonstrated strong recognition of both peptide pulsed fibroblasts as well as transduced fibroblasts in a γ -interferon ELISPOT assay. Figure 2A demonstrates that there was a strong increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts pulsed with the P2S-12 peptide (solid bars) but not with the control E75 peptide (open bars). This shows the ability of these T cells to specifically recognize the P2S-12 peptide. As shown in Figure 2B, this microculture also demonstrated an increase in the number of γ -interferon spots with increasing numbers of T cells on fibroblasts transduced to express the P502S gene but not the HER-2/*neu* gene. These results provide additional confirmatory evidence that the P2S-12 peptide is a naturally processed epitope of the P502S protein. Furthermore, this also demonstrates that there exists in the human T cell repertoire, high affinity T cells which are capable of recognizing this epitope. These T cells should also be capable of recognizing human tumors which express the P502S gene.

EXAMPLE 8

PRIMING OF CTL *IN VIVO* USING NAKED DNA IMMUNIZATION WITH A PROSTATE ANTIGEN

The prostate tumor antigen L1-12, as described above, is also referred to as P501S. HLA A2Kb Tg mice (provided by Dr L. Sherman, The Scripps Research Institute, La Jolla, CA) were immunized with 100 µg VR10132-P501S either intramuscularly or intradermally. The mice were immunized three times, with a two week interval between immunizations. Two weeks after the last immunization, immune spleen cells were cultured with Jurkat A2Kb-P501S transduced stimulator cells. CTL lines were stimulated weekly. After two weeks of *in vitro* stimulation, CTL activity was assessed against P501S transduced targets. Two out of 8 mice developed strong anti-P501S CTL responses. These results demonstrate that P501S contains at least one naturally processed A2-restricted CTL epitope.

EXAMPLE 9

GENERATION OF HUMAN CTL *IN VITRO* USING WHOLE GENE PRIMING AND STIMULATION TECHNIQUES WITH PROSTATE TUMOR ANTIGEN

Using *in vitro* whole-gene priming with P501S-retrovirally transduced autologous fibroblasts (see, for example, Yee et al, *The Journal of Immunology*, 157(9):4079-86, 1996), human CTL lines were derived that specifically recognize autologous fibroblasts transduced with P501S (also known as L1-12), as determined by interferon-γ ELISPOT analysis as described above. Using a panel of HLA-mismatched fibroblast lines transduced with P501S, these CTL lines were shown to be restricted HLA-A2 class I allele. Specifically, dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by growing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, DC were infected overnight with recombinant P501S vaccinia virus at a multiplicity of infection (M.O.I) of five, and matured

overnight by the addition of 3 µg/ml CD40 ligand. Virus was inactivated by UV irradiation. CD8⁺ T cells were isolated using a magnetic bead system, and priming cultures were initiated using standard culture techniques. Cultures were restimulated every 7-10 days using autologous primary fibroblasts retrovirally transduced with P501S. Following four stimulation cycles, CD8⁺ T cell lines were identified that specifically produced interferon-γ when stimulated with P501S-transduced autologous fibroblasts. The P501S-specific activity could be sustained by the continued stimulation of the cultures with P501S-transduced fibroblasts in the presence of IL-15. A panel of HLA-mismatched fibroblast lines transduced with P501S were generated to define the restriction allele of the response. By measuring interferon-γ in an ELISPOT assay, the P501S specific response was shown to be restricted by HLA-A2. These results demonstrate that a CD8⁺ CTL response to P501S can be elicited.

EXAMPLE 10

IDENTIFICATION OF A NATURALLY PROCESSED CTL EPITOPE CONTAINED WITHIN A PROSTATE TUMOR ANTIGEN

The 9-mer peptide p5 (SEQ ID NO: 338) was derived from the P703P antigen (also referred to as P20). The p5 peptide is immunogenic in human HLA-A2 donors and is a naturally processed epitope. Antigen specific CD8⁺ T cells can be primed following repeated *in vitro* stimulations with monocytes pulsed with p5 peptide. These CTL specifically recognize p5-pulsed target cells in both ELISPOT (as described above) and chromium release assays. Additionally, immunization of HLA-A2 transgenic mice with p5 leads to the generation of CTL lines which recognize a variety of P703P transduced target cells expressing either HLA-A2Kb or HLA-A2. Specifically, HLA-A2 transgenic mice were immunized subcutaneously in the footpad with 100 µg of p5 peptide together with 140 µg of hepatitis B virus core peptide (a Th peptide) in Freund's incomplete adjuvant. Three weeks post immunization, spleen cells from immunized mice were stimulated *in vitro* with peptide-pulsed LPS blasts. CTL activity was assessed by chromium release assay five days after primary *in vitro*

stimulation. Retrovirally transduced cells expressing the control antigen P703P and HLA-A2Kb were used as targets. CTL lines that specifically recognized both p5-pulsed targets as well as P703P-expressing targets were identified.

Human *in vitro* priming experiments demonstrated that the p5 peptide is immunogenic in humans. Dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal human donors by culturing for five days in RPMI medium containing 10% human serum, 50 ng/ml human GM-CSF and 30 ng/ml human IL-4. Following culture, the DC were pulsed with p5 peptide and cultured with GM-CSF and IL-4 together with CD8+ T cell enriched PBMC. CTL lines were restimulated on a weekly basis with p5-pulsed monocytes. Five to six weeks after initiation of the CTL cultures, CTL recognition of p5-pulsed target cells was demonstrated.

EXAMPLE 11

EXPRESSION OF A BREAST TUMOR-DERIVED ANTIGEN IN PROSTATE

Isolation of the antigen B305D from breast tumor by differential display is described in US Patent Application No. 08/700,014, filed August 20, 1996. Several different splice forms of this antigen were isolated. The determined cDNA sequences for these splice forms are provided in SEQ ID NO: 366-375, with the predicted amino acid sequences corresponding to the sequences of SEQ ID NO: 292, 298 and 301-303 being provided in SEQ ID NO: 299-306, respectively.

The expression levels of B305D in a variety of tumor and normal tissues were examined by real time PCR and by Northern analysis. The results indicated that B305D is highly expressed in breast tumor, prostate tumor, normal prostate tumor and normal testes, with expression being low or undetectable in all other tissues examined (colon tumor, lung tumor, ovary tumor, and normal bone marrow, colon, kidney, liver, lung, ovary, skin, small intestine, stomach).

EXAMPLE 12

ELICITATION OF PROSTATE TUMOR ANTIGEN-SPECIFIC CTL RESPONSES IN HUMAN BLOOD

This Example illustrates the ability of a prostate tumor antigen to elicit a CTL response in blood of normal humans.

Autologous dendritic cells (DC) were differentiated from monocyte cultures derived from PBMC of normal donors by growth for five days in RPMI medium containing 10% human serum, 50 ng/ml GM-CSF and 30 ng/ml IL-4. Following culture, DC were infected overnight with recombinant P501S-expressing vaccinia virus at an M.O.I. of 5 and matured for 8 hours by the addition of 2 micrograms/ml CD40 ligand. Virus was inactivated by UV irradiation, CD8⁺ cells were isolated by positive selection using magnetic beads, and priming cultures were initiated in 24-well plates. Following five stimulation cycles, CD8⁺ lines were identified that specifically produced interferon-gamma when stimulated with autologous P501S-transduced fibroblasts. The P501S-specific activity of cell line 3A-1 could be maintained following additional stimulation cycles on autologous B-LCL transduced with P501S. Line 3A-1 was shown to specifically recognize autologous B-LCL transduced to express P501S, but not EGFP-transduced autologous B-LCL, as measured by cytotoxicity assays (⁵¹Cr release) and interferon-gamma production (Interferon-gamma Elispot; *see above and Lalvani et al., J. Exp. Med. 186:859-865, 1997*). The results of these assays are presented in Figures 6A and 6B.

EXAMPLE 13

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY MICROARRAY ANALYSIS

This Example describes the isolation of certain prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 372 clones were identified, and 319 were successfully sequenced. Table I presents a summary of these clones, which are shown in SEQ ID NOs:385-400. Of these sequences SEQ ID NOs:386, 389, 390 and 392 correspond to novel genes, and SEQ ID NOs: 393 and 396 correspond to previously identified sequences. The others (SEQ ID NOs:385, 387, 388, 391, 394, 395 and 397-400) correspond to known sequences, as shown in Table I.

Table I
Summary of Prostate Tumor Antigens

Known Genes	Previously identified Genes	Novel Genes
T-cell gamma chain	P504S	23379 (SEQ ID NO:389)
Kallikrein	P1000C	23399 (SEQ ID NO:392)
Vector	P501S	23320 (SEQ ID NO:386)
CGI-82 protein mRNA (23319; SEQ ID NO:385)	P503S	23381 (SEQ ID NO:390)
PSA	P510S	
Ald. 6 Dehyd.	P784P	
L-iditol-2 dehydrogenase (23376; SEQ ID NO:388)	P502S	
Ets transcription factor PDEF (22672; SEQ ID NO:398)	P706P	
hTGR (22678; SEQ ID NO:399)	19142.2, bangur.seq (22621; SEQ ID NO:396)	
KIAA0295(22685; SEQ ID NO:400)	5566.1 Wang(23404; SEQ ID NO:393)	
Prostatic Acid Phosphatase(22655; SEQ ID NO:397)	P712P	
transglutaminase (22611; SEQ ID NO:395)	P778P	
HDLBP (23508; SEQ ID NO:394)		
CGI-69 Protein(23367; SEQ ID NO:387)		
KIAA0122(23383; SEQ ID NO:391)		
TEEG		

CGI-82 showed 4.06 fold over-expression in prostate tissues as

compared to other normal tissues tested. It was over-expressed in 43% of prostate tumors, 25% normal prostate, not detected in other normal tissues tested. L-iditol-2 dehydrogenase showed 4.94 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 90% of prostate tumors, 100% of normal prostate, and not detected in other normal tissues tested. Ets transcription factor PDEF showed 5.55 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% prostate tumors, 25% normal prostate and not detected in other normal tissues tested. hTGR1 showed 9.11 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 63% of prostate tumors and is not detected in normal tissues tested including normal prostate. KIAA0295 showed 5.59 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 47% of prostate tumors, low to undetectable in normal tissues tested including normal prostate tissues. Prostatic acid phosphatase showed 9.14 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 67% of prostate tumors, 50% of normal prostate, and not detected in other normal tissues tested. Transglutaminase showed 14.84 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 30% of prostate tumors, 50% of normal prostate, and is not detected in other normal tissues tested. High density lipoprotein binding protein (HDLBP) showed 28.06 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% of normal prostate, and is undetectable in all other normal tissues tested. CGI-69 showed 3.56 fold over-expression in prostate tissues as compared to other normal tissues tested. It is a low abundant gene, detected in more than 90% of prostate tumors, and in 75% normal prostate tissues. The expression of this gene in normal tissues was very low. KIAA0122 showed 4.24 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 57% of prostate tumors, it was undetectable in all normal tissues tested including normal prostate tissues. 19142.2 bangur showed 23.25 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors and 100% of

normal prostate. It was undetectable in other normal tissues tested. 5566.1 Wang showed 3.31 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 97% of prostate tumors, 75% normal prostate and was also over-expressed in normal bone marrow, pancreas, and activated PBMC. Novel clone 23379 showed 4.86 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in 97% of prostate tumors and 75% normal prostate and is undetectable in all other normal tissues tested. Novel clone 23399 showed 4.09 fold over-expression in prostate tissues as compared to other normal tissues tested. It was over-expressed in 27% of prostate tumors and was undetectable in all normal tissues tested including normal prostate tissues. Novel clone 23320 showed 3.15 fold over-expression in prostate tissues as compared to other normal tissues tested. It was detectable in all prostate tumors and 50% of normal prostate tissues. It was also expressed in normal colon and trachea. Other normal tissues do not express this gene at high level.

EXAMPLE 14

IDENTIFICATION OF PROSTATE TUMOR ANTIGENS BY ELECTRONIC SUBTRACTION

This Example describes the use of an electronic subtraction technique to identify prostate tumor antigens.

Potential prostate-specific genes present in the GenBank human EST database were identified by electronic subtraction (similar to that described by Vasmatzis et al., *Proc. Natl. Acad. Sci. USA* 95:300-304, 1998). The sequences of EST clones (43,482) derived from various prostate libraries were obtained from the GenBank public human EST database. Each prostate EST sequence was used as a query sequence in a BLASTN (National Center for Biotechnology Information) search against the human EST database. All matches considered identical (length of matching sequence >100 base pairs, density of identical matches over this region > 70%) were grouped

(aligned) together in a cluster. Clusters containing more than 200 ESTs were discarded since they probably represented repetitive elements or highly expressed genes such as those for ribosomal proteins. If two or more clusters shared common ESTs, those clusters were grouped together into a "supercluster," resulting in 4,345 prostate superclusters.

Records for the 479 human cDNA libraries represented in the GenBank release were downloaded to create a database of these cDNA library records. These 479 cDNA libraries were grouped into three groups, Plus (normal prostate and prostate tumor libraries, and breast cell lines, in which expression was desired), Minus (libraries from other normal adult tissues, in which expression was not desirable), and Other (fetal tissue, infant tissue, tissues found only in women, non-prostate tumors and cell lines other than prostate cell lines, in which expression was considered to be irrelevant). A summary of these library groups is presented in Table II.

Table II
Prostate cDNA Libraries and ESTs

Library	# of Libraries	# of ESTs
Plus	25	43,482
Normal	11	18,875
Tumor	11	21,769
Cell lines	3	2,838
Minus	166	
Other	287	

Each supercluster was analyzed in terms of the ESTs within the supercluster. The tissue source of each EST clone was noted and used to classify the superclusters into four groups: Type 1- EST clones found in the Plus group libraries only; no expression detected in Minus or Other group libraries; Type 2- EST clones found in the Plus and Other group libraries only; no expression detected in the Minus group; Type 3- EST clones found in the Plus, Minus and Other group libraries, but the

expression in the Plus group is higher than in either the Minus or Other groups; and Type 4- EST clones found in Plus, Minus and Other group libraries, but the expression in the Plus group is higher than the expression in the Minus group. This analysis identified 4,345 breast clusters (*see* Table III). From these clusters, 3,172 EST clones were ordered from Research Genetics, Inc., and were received as frozen glycerol stocks in 96-well plates.

Table III
Prostate Cluster Summary

Type	# of Superclusters	# of ESTs Ordered
1	688	677
2	2899	2484
3	85	11
4	673	0
Total	4345	3172

The inserts were PCR-amplified using amino-linked PCR primers for Synteni microarray analysis. When more than one PCR product was obtained for a particular clone, that PCR product was not used for expression analysis. In total, 2,528 clones from the electronic subtraction method were analyzed by microarray analysis to identify electronic subtraction breast clones that had high tumor vs. normal tissue mRNA. Such screens were performed using a Synteni (Palo Alto, CA) microarray, according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Within these analyses, the clones were arrayed on the chip, which was then probed with fluorescent probes generated from normal and tumor prostate cDNA, as well as various other normal tissues. The slides were scanned and the fluorescence intensity was measured.

Clones with an expression ratio greater than 3 (*i.e.*, the level in prostate tumor cDNA was at least three times the level in normal prostate cDNA) were

identified as prostate tumor-specific sequences (Table IV). The sequences of these clones are provided in SEQ ID NOs:401-453, with certain novel sequences shown in SEQ ID NOs:407, 413, 416-419, 422, 426, 427 and 450.

Table IV
Prostate-tumor Specific Clones

SEQ ID NO.	Sequence Designation	Comments
401	22545	previously identified P1000C
402	22547	previously identified P704P
403	22548	known
404	22550	known
405	22551	PSA
406	22552	prostate secretory protein 94
407	22553	novel
408	22558	previously identified P509S
409	22562	glandular kallikrein
410	22565	previously identified P1000C
411	22567	PAP
412	22568	B1006C (breast tumor antigen)
413	22570	novel
414	22571	PSA
415	22572	previously identified P706P
416	22573	novel
417	22574	novel
418	22575	novel
419	22580	novel
420	22581	PAP
421	22582	prostatic secretory protein 94
422	22583	novel
423	22584	prostatic secretory protein 94
424	22585	prostatic secretory protein 94
425	22586	known
426	22587	novel
427	22588	novel
428	22589	PAP
429	22590	known
430	22591	PSA
431	22592	known
432	22593	Previously identified P777P

433	22594	T cell receptor gamma chain
434	22595	Previously identified P705P
435	22596	Previously identified P707P
436	22847	PAP
437	22848	known
438	22849	prostatic secretory protein 57
439	22851	PAP
440	22852	PAP
441	22853	PAP
442	22854	previously identified P509S
443	22855	previously identified P705P
444	22856	previously identified P774P
445	22857	PSA
446	23601	previously identified P777P
447	23602	PSA
448	23605	PSA
449	23606	PSA
450	23612	novel
451	23614	PSA
452	23618	previously identified P1000C
453	23622	previously identified P705P

EXAMPLE 15

FURTHER IDENTIFICATION OF PROSTATE TUMOR ANTIGENS
BY MICROARRAY ANALYSIS

This Example describes the isolation of additional prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library as described above was screened using microarray analysis to identify clones that display at least a three fold over-expression in prostate tumor and/or normal prostate tissue, as compared to non-prostate normal tissues (not including testis). 142 clones were identified and sequenced. Certain of these clones are shown in SEQ ID NOs:454-467. Of these sequences SEQ ID NOs:459-461 correspond to novel genes. The others (SEQ ID NOs:454-458 and 461-467) correspond to known sequences.

EXAMPLE 16

FURTHER CHARACTERIZATION OF PROSTATE TUMOR ANTIGEN P710P

This Example describes the full length cloning of P710P.

The prostate cDNA library described above was screened with the P710P fragment described above. One million colonies were plated on LB/Ampicillin plates. Nylon membrane filters were used to lift these colonies, and the cDNAs picked up by these filters were then denatured and cross-linked to the filters by UV light. The P710P fragment was radiolabeled and used to hybridize with the filters. Positive cDNA clones were selected and their cDNAs recovered and sequenced by an automatic ABI Sequencer. Four sequences were obtained, and are presented in SEQ ID NOs:468-471.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the present invention is not limited except as by the appended claims.

CLAIMS

1. An isolated polypeptide comprising at least an immunogenic portion of a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(a) sequences recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472;

(b) sequences that hybridize to any of the foregoing sequences under moderately stringent conditions; and

(c) complements of any of the sequence of (a) or (b).

2. An isolated polypeptide according to claim 1, wherein the polypeptide comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotide sequences.

3. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 108, 112, 113, 114, 172, 176, 178, 327, 329, 331, 339 and 383.

4. An isolated polynucleotide encoding at least 15 amino acid residues of a prostate tumor protein, or a variant thereof that differs in one or more

substitutions, deletions, additions and/or insertions such that the ability of the variant to react with antigen-specific antisera is not substantially diminished, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

5. An isolated polynucleotide encoding a prostate tumor protein, or a variant thereof, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing sequences.

6. An isolated polynucleotide comprising a sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

7. An isolated polynucleotide comprising a sequence that hybridizes, under moderately stringent conditions, to a sequence recited in any one of

SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

8. An isolated polynucleotide complementary to a polynucleotide according to any one of claims 4-7.

9. An expression vector comprising a polynucleotide according to any one of claims 4-7.

10. A host cell transformed or transfected with an expression vector according to claim 9.

11. An expression vector comprising a polynucleotide according claim 8.

12. A host cell transformed or transfected with an expression vector according to claim 11.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, in combination with a physiologically acceptable carrier.

14. A vaccine comprising a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

15. A vaccine according to claim 14, wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine according to claim 14, wherein the non-specific immune response enhancer induces a predominantly Type I response.

17. A pharmaceutical composition comprising a polynucleotide according to claim 4, in combination with a physiologically acceptable carrier.

18. A vaccine comprising a polynucleotide according to claim 4, in combination with a non-specific immune response enhancer.

19. A vaccine according to claim 18, wherein the non-specific immune response enhancer is an adjuvant.

20. A vaccine according to claim 18, wherein the non-specific immune response enhancer induces a predominantly Type I response.

21. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a prostate tumor protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472 or a complement of any of the foregoing polynucleotide sequences.

22. A pharmaceutical composition comprising an antibody or fragment thereof according to claim 18, in combination with a physiologically acceptable carrier.

23. A pharmaceutical composition comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a pharmaceutically acceptable carrier or excipient.

24. A pharmaceutical composition according to claim 23, wherein the antigen presenting cell is a dendritic cell or a macrophage.

25. A vaccine comprising an antigen-presenting cell that expresses a polypeptide according to claim 1, in combination with a non-specific immune response enhancer.

26. A vaccine according to claim 25, wherein the non-specific immune response enhancer is an adjuvant.

27. A vaccine according to claim 25, wherein the non-specific immune response enhancer induces a predominantly Type I response.

28. A vaccine according to claim 25, wherein the antigen-presenting cell is a dendritic cell.

29. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

30. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a polynucleotide according to claim 4, and thereby inhibiting the development of a cancer in the patient.

31. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antibody or antigen-

binding fragment thereof according to claim 21, and thereby inhibiting the development of a cancer in the patient.

32. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of an antigen-presenting cell that expresses a polypeptide according to claim 1, and thereby inhibiting the development of a cancer in the patient.

33. A method according to claim 32, wherein the antigen-presenting cell is a dendritic cell.

34. A method according to any one of claims 29-32, wherein the cancer is prostate cancer.

35. A fusion protein comprising at least one polypeptide according to claim 1.

36. A fusion protein according to claim 35, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell transfected with a polynucleotide encoding the fusion protein.

37. A fusion protein according to claim 35, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

38. A fusion protein according to claim 35, wherein the fusion protein comprises an affinity tag.

39. An isolated polynucleotide encoding a fusion protein according to claim 35.

40. A pharmaceutical composition comprising a fusion protein according to claim 32, in combination with a physiologically acceptable carrier.

41. A vaccine comprising a fusion protein according to claim 35, in combination with a non-specific immune response enhancer.

42. A vaccine according to claim 41, wherein the non-specific immune response enhancer is an adjuvant.

43. A vaccine according to claim 41, wherein the non-specific immune response enhancer induces a predominantly Type I response.

44. A pharmaceutical composition comprising a polynucleotide according to claim 40, in combination with a physiologically acceptable carrier.

45. A vaccine comprising a polynucleotide according to claim 40, in combination with a non-specific immune response enhancer.

46. A vaccine according to claim 45, wherein the non-specific immune response enhancer is an adjuvant.

47. A vaccine according to claim 45, wherein the non-specific immune response enhancer induces a predominantly Type I response.

48. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a pharmaceutical composition according to claim 40 or claim 44.

49. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a vaccine according to claim 41 or claim 45.

50. A method for removing tumor cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the prostate tumor protein from the sample.

51. A method according to claim 50, wherein the biological sample is blood or a fraction thereof.

52. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological sample treated according to the method of claim 50.

53. A method for stimulating and/or expanding T cells specific for a prostate tumor protein, comprising contacting T cells with one or more of:

(i) a polypeptide according to claim 1;

(ii) a polypeptide encoded by a polynucleotide comprising a sequence provided in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); and/or

(iv) an antigen presenting cell that expresses a polypeptide of (i) or (ii);

under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

54. An isolated T cell population, comprising T cells prepared according to the method of claim 53.

55. A method for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population according to claim 54.

56. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

(i) a polypeptide according to claim 1;

(ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;

(iii) a polynucleotide encoding a polypeptide of (i) or (ii); or

(iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate; and

(b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient.

57. A method for inhibiting the development of a cancer in a patient, comprising the steps of:

(a) incubating CD4⁺ and/or CD8⁺ T cells isolated from a patient with at least one component selected from the group consisting of:

- (i) a polypeptide according to claim 1;
- (ii) a polypeptide encoded by a polynucleotide comprising a sequence of any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472;
- (iii) a polynucleotide encoding a polypeptide of (i) or (ii); or
- (iv) an antigen-presenting cell that expresses a polypeptide of (i) or (ii);

such that T cells proliferate;

- (b) cloning at least one proliferated cell; and
- (c) administering to the patient an effective amount of the cloned T cells, and thereby inhibiting the development of a cancer in the patient.

58. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence selected from the group consisting of:

(i) polynucleotides recited in any one of SEQ ID NOs: 1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472; and

(ii) complements of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent; and

(c) comparing the amount of polypeptide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

59. A method according to claim 58, wherein the binding agent is an antibody.

60. A method according to claim 59, wherein the antibody is a monoclonal antibody.

61. A method according to claim 58, wherein the cancer is prostate cancer.

62. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of polypeptide that binds to the binding agent;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polypeptide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

63. A method according to claim 62, wherein the binding agent is an antibody.

64. A method according to claim 63, wherein the antibody is a monoclonal antibody.

65. A method according to claim 62, wherein the cancer is a prostate cancer.

66. A method for determining the presence or absence of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and

(c) comparing the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient.

67. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

68. A method according to claim 66, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

69. A method for monitoring the progression of a cancer in a patient, comprising the steps of:

(a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a prostate tumor

protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:1-111, 115-171, 173-175, 177, 179-305, 307-315, 326, 328, 330, 332-335, 340-375, 381, 382 or 384-472, or a complement of any of the foregoing polynucleotides;

(b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide;

(c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and

(d) comparing the amount of polynucleotide detected in step (c) to the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

70. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a polymerase chain reaction.

71. A method according to claim 69, wherein the amount of polynucleotide that hybridizes to the oligonucleotide is determined using a hybridization assay.

72. A diagnostic kit, comprising:

- (a) one or more antibodies according to claim 21; and
- (b) a detection reagent comprising a reporter group.

73. A kit according to claim 72, wherein the antibodies are immobilized on a solid support.

74. A kit according to claim 73, wherein the solid support comprises nitrocellulose, latex or a plastic material.

75. A kit according to claim 72, wherein the detection reagent comprises an anti-immunoglobulin, protein G, protein A or lectin.

76. A kit according to claim 72, wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

77. An oligonucleotide comprising 10 to 40 nucleotides that hybridize under moderately stringent conditions to a polynucleotide that encodes a prostate tumor protein, wherein the tumor protein comprises an amino acid sequence that is encoded by a polynucleotide sequence recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472, or a complement of any of the foregoing polynucleotides.

78. A oligonucleotide according to claim 77, wherein the oligonucleotide comprises 10-40 nucleotides recited in any one of SEQ ID NOs:2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209, 220, 222-225, 227-305, 307-315, 326, 328, 330, 332, 334, 350-365, 381, 382, 384, 386, 389, 390, 392, 393, 396, 401, 402, 407, 408, 410, 413, 415-419, 422, 426, 427, 432, 434, 435, 442-444, 446, 450, 452, 453, 459-461, 468-471 or 472.

79. A diagnostic kit, comprising:

- (a) an oligonucleotide according to claim 77; and
- (b) a diagnostic reagent for use in a polymerase chain reaction or hybridization assay.

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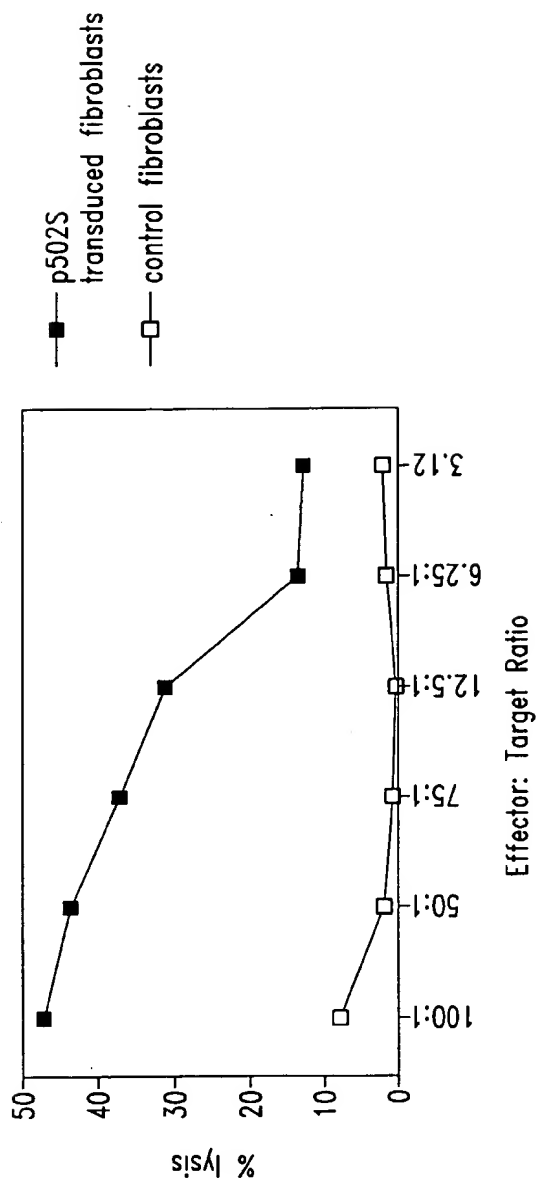
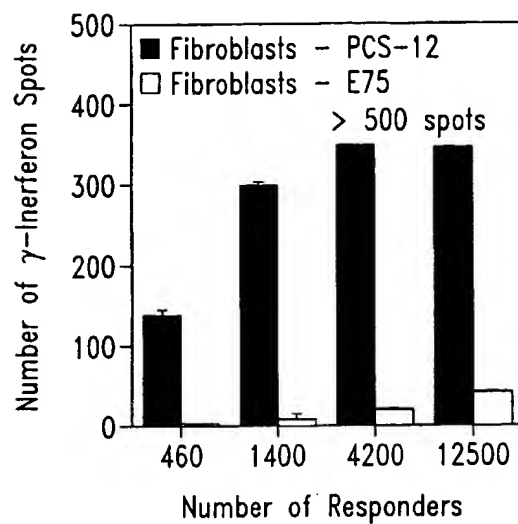
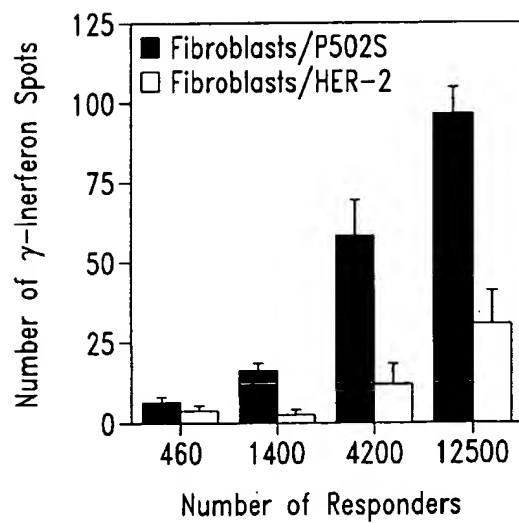


Fig. 1

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*Fig. 2A**Fig. 2B*

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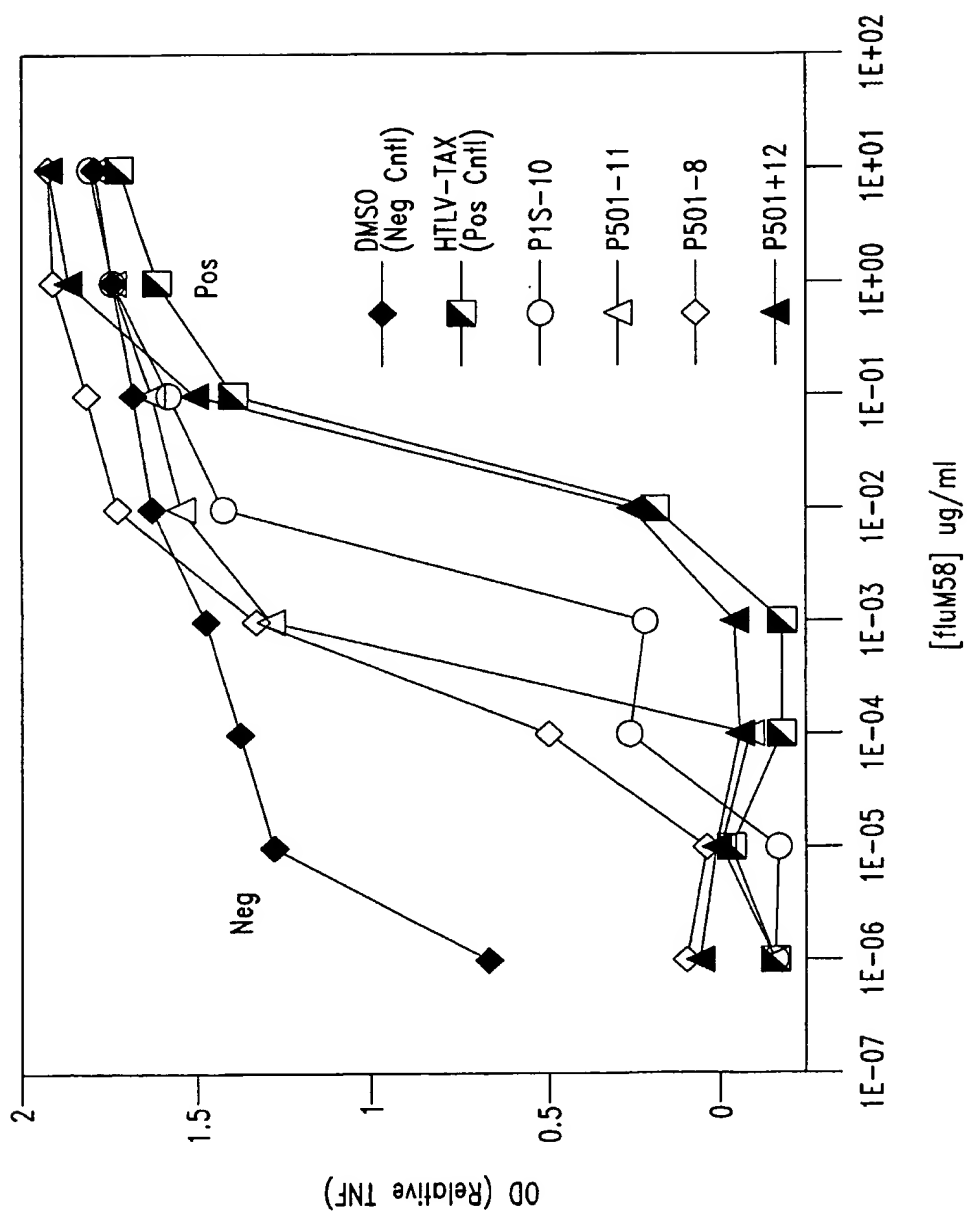


Fig. 3

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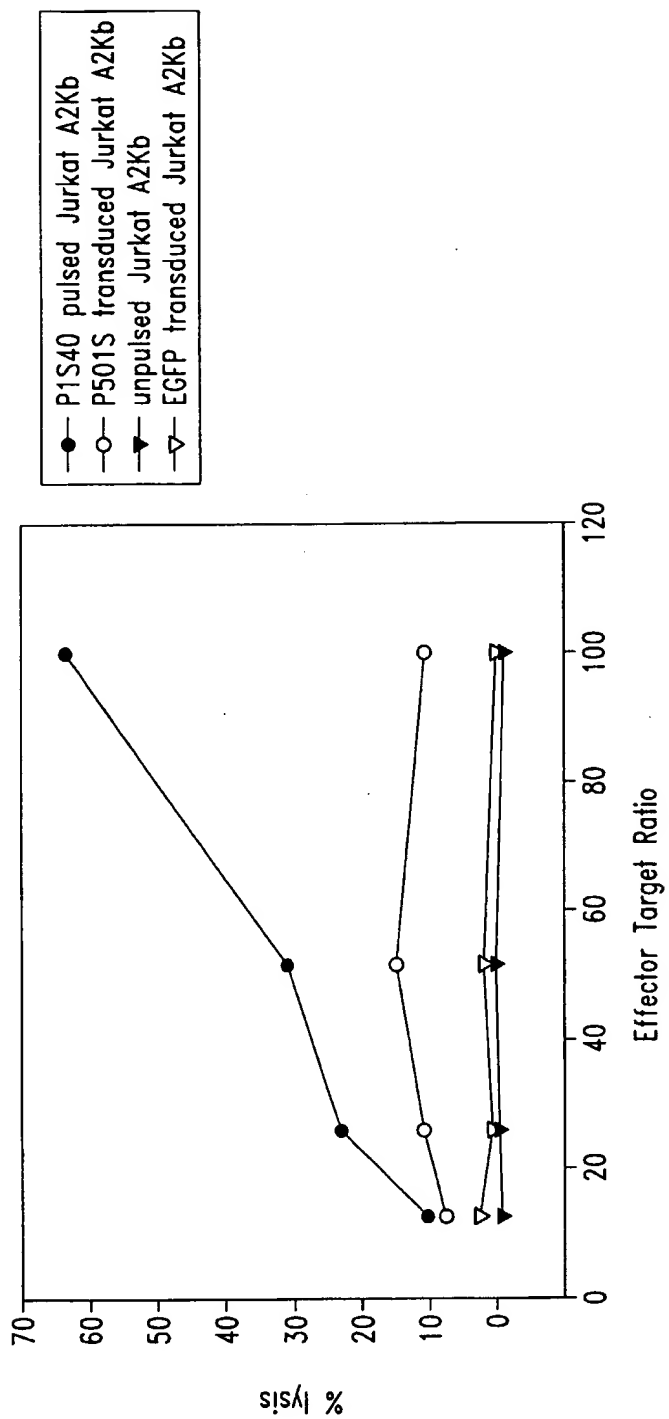
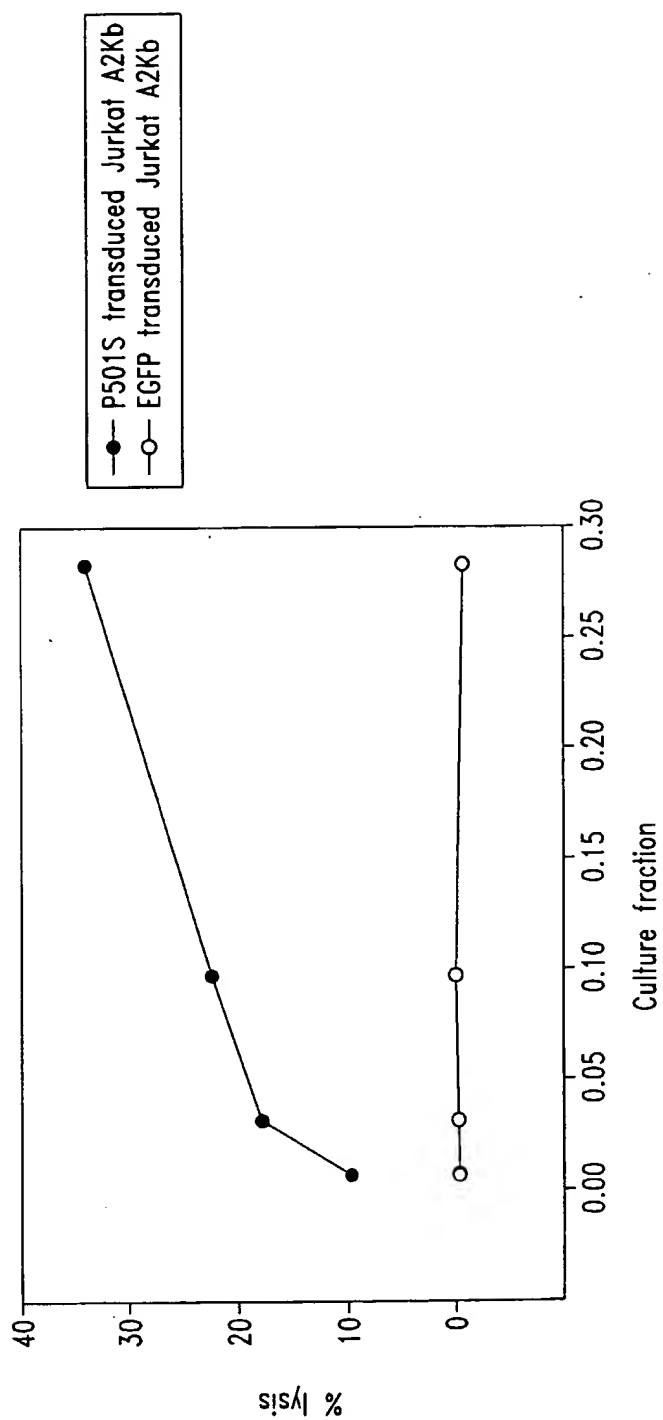
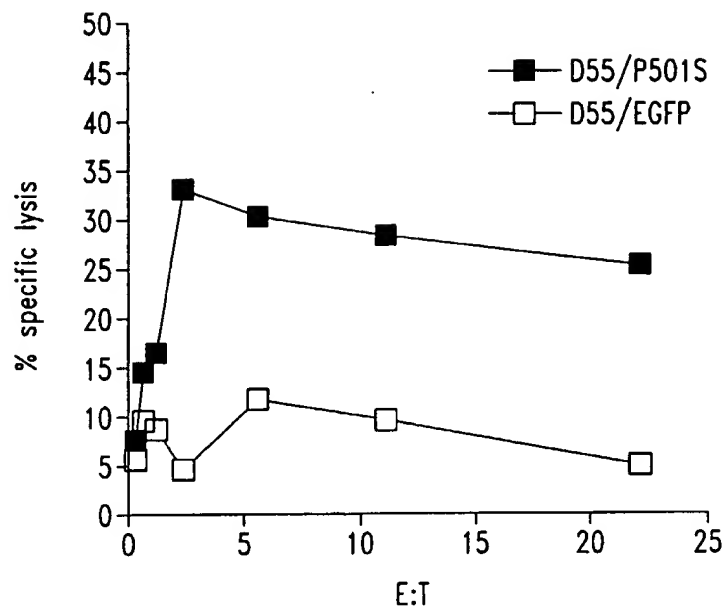
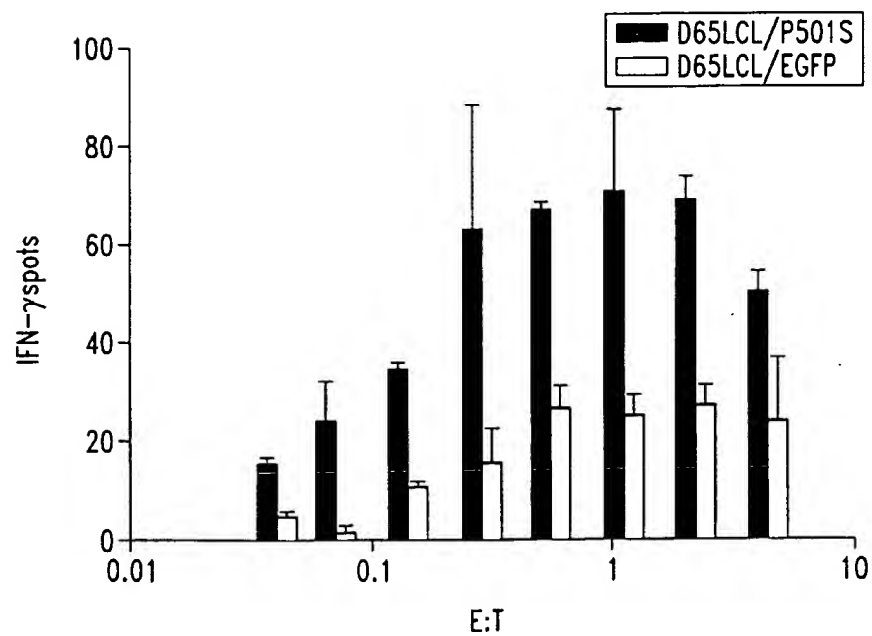


Fig. 4

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*Fig. 5*

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*Fig. 6A**Fig. 6B*

SEQUENCE LISTING

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tccatgtcca	tctgattggg	aagttcatca	gacttttagtc	canntccttt	gatcagcagc	300
tcgtagaact	ggggttctat	tgtctcaaca	gccatgaatt	ccccatctgc	tgctcctgtaa	360
gtcgtataga	aagggtgctcc	accatccaac	atgttctgtc	ctcgaggggg	ggcccggtac	420
ccaattcgcc	ctatantgag	tcgtattacg	cgcgctcact	ggccgctcgt	ttacaacgct	480
gtgactggga	aaaccctggg	cgttaccaac	ttaatcgctt	tgacgacat	ccccctttcg	540
ccagctgggc	gtaatancca	aaaggcccg	accgatcgcc	cttccaacag	ttgcgcacct	600
gaatgggnaa	atgggacccc	cctgttaccg	cgcattnaac	ccccgcnggg	tttngttgtt	660
acccccacnt	nnaccgctta	cactttgcc	gcgccttanc	gcccgcctcc	tttcccttt	720
cttcccttcc	tttccnccn	ctttcccccg	gggtttcccc	cntcaaaccc	cna	773

<210> 4
 <211> 828
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(828)
 <223> n = A,T,C or G

<400> 4						
cctcctgagt	cctactgacc	tgtgctttct	ggtgtggagt	ccagggtctg	taggaaaagg	60
aatgggcaga	cacaggtgta	tgccaatgtt	tctgaaatgg	gtataatttc	gtcctctcct	120
tcggaacact	ggctgtctct	gaagacttct	cgctcagttt	cagtgaggac	acacacaaag	180
acgtgggtga	ccatgttgtt	tgtgggggtc	agagatggga	gggggtgggc	ccaccctgga	240
agagtggaca	gtgacacaag	gtggacactc	tctacagatc	actgaggata	agctggagcc	300
acaatgcatg	aggcacacac	acagcaagga	tgacnctgta	aacatagccc	acgtgtcct	360
gngggcactg	ggaagcctan	atnaggccgt	gagcanaaaag	aaggggagga	tccactagtt	420
ctanagcggc	cgccaccg	gtgganctcc	ancttttgtt	cccttttagt	agggttaatt	480
gcgcgcttgg	cntaatcatg	gtcatanctn	tttctgtgt	gaaattgtta	tccgctcaca	540
attccacaca	acatacganc	cggaacata	aantgtaaac	ctgggggtgc	taatgantga	600
ctaactcaca	ttaattgcgt	tgcgctcact	gcccgccttc	caatcnggaa	acctgtcttg	660
ccncttgcat	tnatgaatcn	gccaaccccc	ggggaaaagc	gtttgcgttt	tgggcgctct	720
tccgcttctc	cnctcantta	ntccctncnc	tcggtcattc	cggtctgcngc	aaaccggttc	780
accnctcca	aagggggtat	tccggtttcc	ccnaatccgg	gganance		828

<210> 5
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

<400> 5
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 agttttaatt gcatccaaag tactaacaaa aactctagca atcaagaatg gcagcatgtt 120
 attttataac aatcaacacc tgtggctttt aaaatttggg tttcataaga taattttatac 180
 tgaagttaat ctagccatgc ttttaaaaaa tgcttttaggt cactccaagc ttggcagtta 240
 acatttgcca taaacaataa taaaacaatc acaattttaat aaataacaaa tacaacattg 300
 taggccataa tcatatacag tataaggaaa aggtggtagt gttgagtaag cagttattag 360
 aatagaatac cttggcctct atgcaaatac gtctagacac tttgattcac tcagccctga 420
 cattcagttt tcaaagtagg agacaggttc tacagtatca ttttacagtt tccaacacat 480
 tgaaaacaag tagaaaatga tgagttgatt tttattaatg cattacatcc tcaagagtta 540
 tcaccaaccc ctacagttata aaaaattttc aagtttatatt agtcatataa cttgggtgtgc 600
 ttattttaaa ttagtgctaa atggattaag tgaagacaac aatgggtcccc taatgtgatt 660
 gatattgggc atttttacca gcttctaaat ctnaacttcc aggcctttga actggaacat 720
 tgnatnacag tgttccanag ttncaaccta ctggaacatt acagtgtgct tgattcaaaa 780
 tgttattttg ttaaaaatta aattttaacc tgggtgaaaa ataatttgaa atna 834

<210> 6
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 6
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 aaccacatct acaaaatgcc agtatcaggc ggcggcttcg aagccaaagt gatgtttgga 120
 tgtaaaagtga aatattagtt ggcggatgaa gcagatagtg aggaaagtgt agccaataat 180
 gacgtgaaagt ccgtggaagc ctgtggctac aaaaaatgtt gagccgtaga tgccgtcgga 240
 aatgggtgaag ggagactcga agtactctga ggcttgtagg agggtaaaat agagaccag 300
 taaaattgta ataagcagtg cttgaattat ttggtttcgg ttgttttcta ttagactatg 360
 gtgagctcag gtgattgata ctccgtatgc gagtaatacg gatgtgttta ggagtgaggac 420
 ttctagggga tttagcgggg tgatgcctgt tggggggccag tgccctccta gttggggggt 480
 aggggctagg ctggagtggg aaaaggctca gaaaaatcct gcgaagaaaa aaacttctga 540
 ggtaataaat aggattatcc cgtatcgaag gccttttttg acaggtggtg tgtggtggcc 600
 ttggtatgtg ctttctcgtg ttacatcgcg ccattcattg tatatgggta gtgtgttggg 660
 ttantanggc ctantatgaa gaacttttgg antggaatta aatcaatngc ttggccggaa 720
 gtcattanga nggctnaaaa ggccctgtta ngggtctggg ctnggtttta ccnaccat 780
 ggaatncccc ccccggaacna ntgnatccct attcttaa 818

<210> 7
 <211> 817
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(817)
 <223> n = A,T,C or G

<400> 7
 tttttttttt tttttttttt tggctctaga gggggtagag ggggtgctat agggtaaata 60
 cgggccctat ttcaaagatt tttaggggaa ttaattctag gacgatgggt atgaaactgt 120
 ggtttgctcc acagatttca gagcattgac cgtagtatac ccccggtcgt gtagcggtaga 180

aagtggtttg	gtttagacgt	ccgggaattg	catctgtttt	taagccta	gtggggacag	240
ctcatgagtg	caagacgtct	tgtgatgtaa	ttattatacn	aatgggggct	tcaatcggga	300
gtactactcg	attgtcaacg	tcaaggagtc	gcaggtcgcc	tggttctagg	aataatgggg	360
gaagtatgta	ggaattgaag	attaatccgc	cgtagtcggt	gttctcctag	gttcaatacc	420
attggtggcc	aattgatttg	atggtaaggg	gagggatcgt	tgaactcgtc	tggtatgtaa	480
aggatncctt	ngggatggga	aggcnatnaa	ggactangga	tnaatggcgg	gcangatatt	540
tcaaacngtc	tctanttcct	gaaacgtctg	aaatgtta	aanaattaa	tttngttatt	600
gaatnttnng	gaaaagggct	tacaggacta	gaaaccaa	angaaaanta	atnntaangg	660
cnttatcntn	aaaggnata	accnctccta	tnatcccacc	caatngnatt	ccccacncnn	720
acnattggat	nceccanttc	canaaanggc	cncccccg	tgannccnc	cttttgttcc	780
cttnantgan	ggttattcnc	ccctngcntt	atcance			817

<210> 8

<211> 799

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(799)

<223> n = A,T,C or G

<400> 8

catttccggg	tttactttct	aaggaaagcc	gagcggaagc	tgctaacgtg	ggaatcgggtg	60
cataaggaga	actttctgct	ggcacgcgct	agggacaagc	gggagagcga	ctccgagcgt	120
ctgaagcgca	cgtcccagaa	ggtggacttg	gcaactgaa	agctgggaca	catccgcgag	180
tacgaacagc	gcctgaaagt	gctggagcgg	gaggtccagc	agtgtagccg	cgtcctgggg	240
tgggtggccg	angcctganc	cgtctgcct	tgctgcccc	angtgggccc	ccacccccctg	300
acctgcctgg	gtccaaacac	tgagccctgc	tgggcgactt	caagganaac	ccccacangg	360
ggattttgct	cctanantaa	ggctcatctg	ggcctcggcc	ccccacactg	gttggccttg	420
tctttgagnt	gagccccatg	tccatctggg	ccactgtcng	gaccaccttt	ngggagtgtt	480
ctccttacaa	ccacannatg	cccggctcct	cccgaaacc	antccancc	tgngaaggat	540
caagnctcgn	atccactnnt	nctanaaccg	gcncncnccg	cngtggaa	cnccttntgt	600
tccttttcnt	tnagggttaa	tnnccgcttg	gccttnccan	ngtcctncnc	nttttccnnt	660
gttnaaattg	ttangcnccc	nccnntcccn	cnnnncnanc	cccgaccnnc	annttnnann	720
ncctgggggt	nccnncngat	tgaccnnc	nccctntant	tgcnttnggg	nncnntgccc	780
ctttccctct	nggganncg					799

<210> 9

<211> 801

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(801)

<223> n = A,T,C or G

<400> 9

acgccttgat	cctcccaggc	tgggactggt	tctgggagga	gccgggcatg	ctgtggtttg	60
taangatgac	actcccaaag	gtggtcctga	cagtggccca	gatggacatg	gggctcacct	120
caaggacaag	gccaccaggt	gcggggccg	aagccacat	gatccttact	ctatgagcaa	180
aatccctgt	gggggcttct	ccttgaagtc	cgccancagg	gctcagctt	tggacccang	240
caggtcatgg	ggttgtngnc	caactggggg	cncaacgca	aaanggcnc	gggcctcngn	300
caccocatcc	angacggcgc	tacactnctg	gacctccnc	tccaccactt	tcatgcgctg	360
ttcntaccgg	cgnatntgtc	ccanctgttt	cngtgcenac	tccancttct	nggacgtgcg	420
ctacatacgc	ccggantcnc	netcccgctt	tgteccctatc	cacgtncan	caacaaattt	480
cncntantg	caccnatcc	cacttttnc	agntttccnc	nncgngcttc	cttntaaaag	540
ggttganc	cggaaaatnc	cccaaagggg	gggggcngg	taccaaactn	ccccnata	600
gctgaantcc	ccatnaccnn	gnctcnatgg	ancntccnt	tttaannacn	ttctnaactt	660
gggaananc	ctcgnccntn	ccccnttaa	tccncccttg	cnangnnct	ccccnntcc	720
nccnnntng	gcntntnann	cnaaaaaggc	cnnnancaa	tctcctnn	cctcanttcg	780

ccanccctcg aaatcgccn c

801

<210> 10
 <211> 789
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(789)
 <223> n = A,T,C or G

<400> 10
 cagtctatnt ggccagtgtg gcagctttcc ctgtggctgc cgggtgccaca tgcctgtccc 60
 acagtgtggc cgtgggtgaca gcttcagccg ccctcaccgg gttcaccttc tcagccctgc 120
 agatccctgc ctacacactg gcctccctct accaccggga gaagcagggtg ttctgtccca 180
 aataccgagg ggacactgga ggtgctagca gtgaggacag cctgatgacc agcttcctgc 240
 caggccctaa gcctggagct cccttcccta atggacacgt ggggtgctgga ggcagtggcc 300
 tgctcccacc tccaccgcg ctctgcgggg cctctgcctg tgatgtctcc gtacgtgtgg 360
 tggtgggtga gccaccgan gccagggtgg ttccggggccg gggcatctgc ctggacctgc 420
 ccctccctga tagtgcttcc tgctgtccca nggtggccca tccctgttta tgggtccat 480
 tgtccagctc agccagtctg tcaactgccta tatggtgtct gccgcaggcc tgggtctggt 540
 cccatttact ttgctacaca ggtantattt gacaagaacg anttggccaa atactcagcg 600
 ttaaaaaatt ccagcaacat tgggggtgga aggcctgcct cactgggtcc aactccccgc 660
 tctgtttaac cccatggggc tgccggcttg gccgccaatt tctgttgctg ccaaantnat 720
 gtggctctct gctgccacct gttgctggct gaagtgcnta cngcncanct nggggggtng 780
 gnggttccc 789

<210> 11
 <211> 772
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(772)
 <223> n = A,T,C or G

<400> 11
 cccaccctac ccaaatatta gacaccaaca cagaaaagct agcaatggat tcccttctac 60
 tttgttaaat aaataagtta aatattttaa tgcctgtgtc tctgtgatgg caacagaagg 120
 accaacaggc cacatccctga taaaaggtaa gaggggggtg gatcagcaaa aagacagtgc 180
 tgtgggctga ggggacctgg ttcttgtgtg ttgcccctca ggactcttcc cctacaaata 240
 actttcatat gttcaaattcc catggaggag tgtttcatcc tagaaactcc catgcaagag 300
 ctacattaaa cgaagctgca ggtaagggg cttanagatg ggaaaccagg tgactgagtt 360
 tattcagctc ccaaaaaccc ttctctaggt gtgtctcaac taggaggcta gctgttaacc 420
 ctgagcctgg gtaatccacc tgcagagtcc ccgcattcca gtgcatggaa cccttctggc 480
 ctccctgtat aagtccagac tgaaaccccc ttggaaggnc tccagtccagg cagccctana 540
 aactggggaa aaaagaaaag gacgccccan ccccagctg tgcantacg cacctcaaca 600
 gcacagggtg gcagcaaaaa aaccatttta ctttggcaca aacaaaaact ngggggggca 660
 accccggcac cccnangggg gttaacagga ancngggnaa cntggaaccc aattnaggca 720
 ggcccncac ccnaatntt gctgggaaat ttttctctcc ctaaattntt tc 772

<210> 12
 <211> 751
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(751)
 <223> n = A,T,C or G


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<400> 12
gccccaatc cagctgccac accacccacg gtgactgcat tagttcggat gtcatacaaa 60
agctgattga agcaaccctc tacttttttg tcgtgagcct tttgcttggt gcaggtttca 120
ttggctgtgt tggtagcgtt gtcattgcaa cagaatgggg gaaaggcact gttctctttg 180
aagtanggtg agtccctcaa atccgtatag ttggtgaagc cacagcactt gagccctttc 240
atggtggtgt tccacacttg agtgaagtct tcctgggaac cataatcttt cttgatggca 300
ggcactacca gcaacgtcag ggaagtgtc agccattgtg gtgtacacca aggcgaccac 360
agcagctgcn acctcagcaa tgaagatgan gaggangatg aagaagaacg tcncgagggc 420
acacttgctc tcagtcttan caccatanca gcccntgaaa accaananca aagaccacna 480
cnccggctgc gatgaagaaa tnaccccneg ttgacaaact tgcattggcag tggganccac 540
agtggcccn aaaaattcttca aaaaggatgc cccatcnatt gaccccccaa atgcccactg 600
ccaacagggg ctgccccacn cncnnaacga tganccnatt gnacaagatc tncntggtct 660
tnatnaacnt gaacctgcn tngtggctcc tggtcaggnc cnnggcctga cttctnaann 720
aangaactcn gaagncccca cngganannc g 751

```

```

<210> 13
<211> 729
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(729)
<223> n = A,T,C or G

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<400> 13
gagccaggcg tccctctgcc tgcccactca gtggcaacac ccgggagctg ttttgcctt 60
tgtggancct cagcagtncc ctctttcaga actcantgcc aaganccctg aacaggagcc 120
accatgcagt gcttcagctt cattaagacc atgatgatcc tcttcaattt gctcatcttt 180
ctgtgtggtg cagccctgtt ggcagtgggc atctgggtgt caatcgatgg ggcacacctt 240
ctgaagatct tcgggccact gtcgtccagt gccatgcagt ttgtcaacgt gggctacttc 300
ctcatcgcat ccggcggtgt ggtcttagct ctaggtttcc tgggctgcta tgggtgctaag 360
actgagagca agtgtgccct cgtgacgttc ttcttcaccc tcctctcatc cttcattgct 420
gaggttgcaa tgctgtggtc gccttggtgt acaccacaat ggctgagcac ttctgacgt 480
tgctggtaat gcctgccatc aanaaaagat tatgggttcc caggaanact tcaactcaagt 540
gttggaacac caccatgaaa gggctcaagt gctgtggctt cnnccaacta tacggatttt 600
gaagantcac ctacttcaaa gaaaanagtg cctttccccc atttctgttg caattgacaa 660
acgtccccaa cacagccaat tgaaaacctg caccacaacc aaanggggtcc ccaaccanaa 720
attnaaggg 729

```

```

<210> 14
<211> 816
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(816)
<223> n = A,T,C or G

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```

<400> 14
tgctcttctt caaagttgtt cttgttgcca taacaaccac cataggtaaa gcgggagcag 60
tggtcgctga aggggttcta gtaccagcgc gggatgctct ccttgagag tcctgtgtct 120
ggcaggtcca cgcagtgcc tttgtcactg gggaaatgga tgctgtgag ctgctcaaag 180
ccactcggtt atttttcaca ggcagcctcg tccgacgcgt cggggcagtt gggggtgtct 240
tcacactcca ggaaactgtc natgcagcag ccattgctgc agcggaactg ggtgggctga 300
cangtgccag agcacactgg atggcgctt tccatggnan gggccctgng ggaaagtccc 360
tganccccc anctgctct caaangcccc accttgaca ccccgacagg ctagaatgga 420
atcttcttcc cgaaagtag tnttcttgt tgcccaancc ancccntaa acaaaactctt 480
gcanatctgc tccngggggg tentantacc ancggtggaa aagaacccca ggcnegcgaac 540
caancttgtt tggatnagaa gcnataatct nctnttctgc ttggtggaca gcaccantna 600

```

ctgtnnanct	ttagnccntg	gtcctcntgg	gttggncttg	aacctaatcn	ccnntcaact	660
gggacaaggt	aantngccnt	ccttttnaatt	cccnancntn	ccccctgggt	tgggggttttn	720
cncnctccta	ccccagaaan	nccgtgttcc	cccccaacta	ggggccnaaa	ccnntnttcc	780
cacaaccctn	ccccacccac	gggttcngnt	ggttng			816

<210> 15
 <211> 783
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(783)
 <223> n = A,T,C or G

<400> 15						
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atgtggaaaa	cacagattgg	cgccactgac	ggggtgacac	ggatgtcagg	gtagagagga	120
aagacccaaa	ccaggtggaa	ctgtggggac	tcaaggaang	cacctacctg	ttccagctga	180
cagtgcactg	ctcagaccac	ccagaggaca	cggccaaact	cacagtcaact	gtgctgtcca	240
ccaagcagac	agaagactac	tgccctcgcat	ccaacaangt	gggtcgctgc	cggggctctt	300
tcccacgctg	gtactatgac	cccacggagc	agatctgcaa	gagtttctgt	tatggaggct	360
gcttggggcaa	caagaacaac	taccttcggg	aagaagagt	cattctancc	tgctnggggtg	420
tgcaagggtg	gcctttgana	ngcanctctg	gggctcangc	gactttcccc	cagggccccct	480
ccatggaaa	gcgccatcca	ntgttctctg	gcacctgtca	gccccaccag	ttccgctgca	540
ncaatggctg	ctgcactnac	antttcctng	aattgtgaca	acacccccca	ntgcccccaa	600
ccctcccaac	aaagcttccc	tgtnnaaaaa	tacnccant	ggcttttnac	aaacncccg	660
cncctccntt	ttccccnntn	aacaaagggc	nctngcnttt	gaactgccc	aacccnggaa	720
tctnccnngg	aaaaantncc	ccccctgggt	cctnnaancc	cctccncaaa	anctncccc	780
ccc						783

<210> 16
 <211> 801
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(801)
 <223> n = A,T,C or G

<400> 16						
gccccaatc	cagctgccac	accacccacg	gtgactgcat	tagttcggat	gtcatataaa	60
agctgattga	agcaaccctc	tacttttttg	tcgtgagcct	tttgcttggt	gcagggtttca	120
ttggctgtgt	tggtgacgtt	gtcattgcaa	cagaatggg	gaaaggcact	gttctctttg	180
aagtaggggtg	agtcctcaaa	atccgtatag	ttggtgaagc	cacagcactt	gagccctttc	240
atgggtggtg	tccacacttg	agtgaagtct	tcttggaac	cataatcttt	cttgatggca	300
ggcactacca	gcaacgtcag	gaagtgtca	gccattgtg	tgtacaccaa	ggcgaccaca	360
gcagctgcaa	cctcagcaat	gaagatgagg	aggaggatga	agaagaacgt	cncgagggca	420
cacttgctct	ccgtcttagc	accatagcag	cccangaaac	caagagcaaa	gaccacaacg	480
ccngctgcga	atgaaagaaa	ntacccacgt	tgacaaactg	catggccact	ggacgacagt	540
tggtccgaan	atcttcagaa	aagggatgcc	ccatcgattg	aacacccana	tgcccactgc	600
cnacagggct	gcncncncn	gaaagaatga	gccattgaag	aaggatcntc	ntggctcttaa	660
tgaactgaaa	ccntgcatgg	tggtccctgt	tcagggtctc	tggcagtga	ttctganaaa	720
aaggaacngc	ntnagcccc	ccaaangana	aaacaccccc	gggtgttgcc	ctgaattggc	780
ggccaaggan	ccctgccccn	g				801

<210> 17
 <211> 740
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(740)
 <223> n = A,T,C or G

<400> 17
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 cctttgtgga gcctcagcag ttccctcttt cagaactcac tgccaagagc cctgaacagg 120
 agccaccatg cagtgttca gcttcattaa gaccatgatg atcctcttca atttgcctcat 180
 ctttctgtgt ggtgcagccc tgttggcagt gggcatctgg gtgtcaatcg atggggcatc 240
 ctttctgaag atcttcgggc cactgtcgtc cagtgccatg cagtttgtca acgtgggcta 300
 cttcctcatc gcagccggcg ttgtggtctt tgctcttggg ttccctgggct gctatgggtc 360
 taagacggag agcaagtgtg ccctcgtgac gttcttcttc atcctcctcc tcatcttcat 420
 tgctgaagtt gcagctgctg tggtcgcctt ggtgtacacc acaatggctg aaccattcct 480
 gacgttgctg gtantgcctg ccatcaanaa agattatggg ttcccaggaa aaattcactc 540
 aantntggaa caccnccatg aaaagggctc caatttctgn tggcttcccc aactataccg 600
 gaattttgaa agantcnccc tacttccaaa aaaaaanant tgccttttnc cccnttctgt 660
 tgcaatgaaa acntcccaan acngccaatn aaaacctgcc cnnncaaaaa ggntcncaaa 720
 caaaaaaant nnaagggttn 740

<210> 18
 <211> 802
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(802)
 <223> n = A,T,C or G

<400> 18
 ccgctgggtg cgtgtgtcca gngnagccac gaagcacgtc agcatacaca gcctcaatca 60
 caaggtcttc cagctgccgc acattacgca gggcaagagc ctccagcaac actgcataatg 120
 ggatacactt tactttagca gccagggtga caactgagag gtgtcgaagc ttattcttct 180
 gagcctctgt tagtgaggga agattccggg cttcagctaa gtatgcagcg tatgtcccat 240
 aagcaaacac tgtgagcagc cggaaggtag aggcaaagtc actctcagcc agctctctaa 300
 cattgggcat gtccagcagt tctccaaaca cgtagacacc agnggcctcc agcacctgat 360
 ggatgagtggt ggccagcgct gccccttgg cgcacttggc taggagcaga aattgctcct 420
 ggttctgccc tgtcaccttc acttcgcac tcactactgc actgagtgtg ggggacttgg 480
 gctcaggatg tccagagacg tggttccgcc cctcncctta atgacaccgn ccanncaacc 540
 gtcggctccc gccgantgng ttcgtcgtnc ctgggtcagg gtctgctggc cnctacttgc 600
 aancttcgtc nggcccatgg aattcacnnc accggaactn gtangatcca ctnttctat 660
 aaccgngcgc caccgcnntt ggaactccac tcttnttnc tttacttgag ggtaaggtc 720
 acccttnnccg ttaccttggg ccaaaccntn cntgtgtcg anantngtna tcnngnccna 780
 tnccanccnc atangaagcc ng 802

<210> 19
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 19
 cnaagcttcc aggtnacggg ccgcnancc tgaccnagg tancanaang cagnncgagg 60
 gagccacccg tcacngngng gngtctttat nggagggggc ggagccacat cntggacnt 120
 cntgacccca actcccccc ncnantgca gtgatgagtg cagaactgaa ggtnacgtgg 180
 caggaaccaa gancaaannc tgctccnntc caagtcggcn nagggggcgg ggctggccac 240
 gcncatccnt cnagtgtctn aaagccccc cctgtctact tgtttggaga acngcnnga 300

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catgcccagn gttanataac nggcngagag tnanntttgcc tctcccttcc ggctgcgcan 360
cgngtntgct tagnggacat aacctgacta cttactgaa cccnngaac tncnccccct 420
ccactaagct cagaacaaaa aacttcgaca ccactcantt gtcacctgnc tgctcaagta 480
aagtgtaccc catncccaat gtntgctnga ngctctgncc tgcnttangt tcggctcctgg 540
gaagacctat caattnaagc tatgtttctg actgcctctt gctccctgna acaancnacc 600
cnnnntcca aggggggggnc ggcccccaat ccccccaacc ntnaattnan tttancccn 660
ccccnggcc cggcctttta cnancntcnn nnaacnggna aaaccnnngc ttncccaac 720
nnaatcncc t 731

```

```

<210> 20
<211> 754
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(754)
<223> n = A,T,C or G

```

```

<400> 20
tttttttttt tttttttttt taaaaacccc ctccattnaa tgnaaacttc cgaaattgtc 60
caacccccctc ntccaaatnn cnttttccgg gnggggggttc caaacccaan ttanntttgg 120
annttaaatt aaatnttntt tggnggnna anccnaatgt nangaaagt naaccanta 180
tnancttnaa tncctggaaa ccngtngntt ccaaaaatnt ttaaccctta antccctccg 240
aaatngttna nggaaaaccc aanttctcnt aaggttggtt gaaggttnaa tnaaaanccc 300
nnccaattgt ttttngccac gcctgaatta attggnntcc gntgttttcc nttaaaanaa 360
ggnnancccc ggttantnaa tcccccnnc ccaattata ccgantttt ttngaattgg 420
gancccnccg gaattaacgg ggnnntccc tnttgggggg cnggnncccc cccntcggg 480
ggttngggnc aggnennaat tgtttaaggg tccgaaaaat ccctccnaga aaaaaanctc 540
ccagngtgag nntngggtt ncccccccc canggccct ctcgnanaag tggggtttgg 600
ggggcctggg atttntttc cctnttnc tcccccccc ccnggganag aggttngnt 660
tttntcnnn ggcccnccn aagancttn ccganttna ttaaatecnt gcctnggcga 720
agtccttgn agggntaaan ggccccctnn cggg 754

```

```

<210> 21
<211> 755
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(755)
<223> n = A,T,C or G

```

```

<400> 21
atcancccat gacccnaac nngggaccnc tcancggnc nnncnaccnc cggccnatca 60
nngtnagnnc actncnntn natcacnccc cncnactac gcccnananc cnacgncta 120
nncanatncc actganngcg cgangtngan ngagaaanct nataccanag naccanacn 180
ccagctgtcc nanaangcct nnnatacngg nnnatccaat ntgnancctc cnaagtattn 240
nncnncanat gattttcctn anccgattac cntncccc tanccctcc ccccaacna 300
cgaaggcnct ggncnaagg nngcgnccc ccgctagntc ccnncaagt cncnnccta 360
aactcancn nattacnccg ttctgagta tcactcccc aatctcacc tactcaactc 420
aaaaanaten gatacaaat aatncaagcc tgnttatnac actntgactg ggtctctatt 480
ttagnggtcc ntnaancntc ctaatactc cagtcnccct tcnccaatt ccnaanggt 540
ctttcngaca gcatntttt gttcccnntt gggttcttan ngaattgcc ttcntngaac 600
gggctcntct tttccttcgg ttanccctgg tcnncggc cagttattat tcccntttt 660
aaattcntnc cntttanttt tggcnttca aacccccggc cttgaaaacg gccccctggt 720
aaaaggttgt tttganaaaa ttttgtttt gttcc 755

```

```

<210> 22
<211> 849
<212> DNA

```

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(849)

<223> n = A,T,C or G

<400> 22

tttttttttt	tttttangtg	tngtcgtgca	ggtagaggct	tactacaant	gtgaanacgt	60
acgctnggan	taangcgacc	cganttctag	ganncnccct	aaaatcanac	tgtgaagatn	120
atcctgnnna	cggaanggtc	accggnngat	nntgctaggg	tgncnctcc	cannncnttn	180
cataactcng	nggccctgcc	caccaccttc	ggcgggccng	ngnccgggcc	cgggtcattn	240
gnnttaaccn	cactnngcna	ncggtttccn	ncnccnncng	accnngcgga	tccgggggtnc	300
tctgtcttcc	cctgnagncn	anaaantggg	ccnccggnccc	ctttaccctt	nnacaagcca	360
cngccntcta	ncnccngccc	cccctccant	nngggggact	gccnanngct	ccgttntctng	420
nnaccccnnn	gggtncctcg	gttgctcgant	cnaccgnang	ccanggattc	cnaaggaagg	480
tgcgttnttg	gcccctaccc	ttcgtcncgg	nncacccttc	ccgacnanga	nccgctcccg	540
cncnccgnng	cctcncctcg	caacacccgc	notctcngt	ncggnnnccc	ccccacccgc	600
ncctcncnc	ngnccgnancn	ctcncnccc	gtctcannca	ccaccccgcc	ccgccaggcc	660
ntcanccacn	ggnggacnng	nagcncnntc	gcncccgcgn	gcgnccctt	cgccncngaa	720
ctnctcngg	ccantnncgc	tcaanccnna	cnaaacgcgc	ctgcgcggcc	cgnagcgncc	780
ncctcncga	gtcctcccgn	cttcncccc	angnttccn	cgaggacacn	nnaccccgcc	840
nncangcgg						849

<210> 23

<211> 872

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(872)

<223> n = A,T,C or G

<400> 23

gcgcaaaacta	tacttcgctc	gnactcgtgc	gcctcgtcnc	tcttttcctc	cgcaaccatg	60
tctgacnanc	ccgattnggc	ngatatchan	aagntcganc	agtccaaact	gantaacaca	120
cacacnncn	aganaaatcc	nctgccttcc	anagtanacn	attgaacnng	agaaccangc	180
nggcgaatcg	taatnaggcg	tgcgcgcgca	atntgtcnc	gtttattntn	ccagctcnc	240
ctnccnacc	tactcttcn	nagctgtcnn	accctngtn	cgnaccccc	naggtcgga	300
tgcgggtttn	nntgaccgng	cnccccctcc	ccccntccat	nacganccnc	ccgcaccacc	360
nanngcncgc	ncnccgnnct	cttcgcnc	ctgtcctntn	cccctgtngc	ctggcncngn	420
accgcattga	ccctcgccnn	ctncnngaaa	ncgnanacgt	ccgggttggn	annancgctg	480
tgggnnngcg	tctgcncgc	gttccttcn	ncncttcca	ccatcttctt	taenggtct	540
ccnccgcntc	tcnnncacnc	cctgggacgc	tntcctntgc	cccccttnac	tccccctt	600
cgnccgtgnc	cgnccccacc	ntcatttnca	nacgntcttc	acaannncct	ggntnnctcc	660
cnancngncn	gtcanccnag	ggaaggngg	ggnnccnntg	nttgacgttg	nggngangtc	720
cgaanantcc	tcnccntcan	cctaccct	cgggcgnnct	ctcngttnc	aacttancaa	780
ntctcccccg	ngngcncntc	tcagcctcnc	cnccccnct	ctctgcantg	tntctgctc	840
tnaccnntac	gantnttcgn	cncctcttt	cc			872

<210> 24

<211> 815

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(815)

<223> n = A,T,C or G

<400> 24

gcattgcaagc	ttgagtattc	tatagngtca	cctaaatanc	ttggcntaat	catggtcnta	60
nctgncttcc	tgtgtcaa	gtatacnaa	tanatatgaa	tctnatntga	caaganngta	120
tcntncatta	gtaacaantg	tnntgtccat	cctgtengan	canattccca	tnnattnecn	180
cgcattcnch	gcncantatn	taatngggaa	ntcnntnnn	ncaccnncat	ctatcntncc	240
gcnccttgac	tggagagat	ggatnanttc	tnntntgacc	nacatgttca	tcttggattn	300
aananccecc	cgengnccac	cggttngnng	cnagecnntc	ccaagacctc	ctgtggagggt	360
aacctgctgc	aganncatca	aacntgggaa	acccgcnncc	angtnnaagt	ngnnncanan	420
gateccgtcc	aggnttnacc	atcccttcnc	agcgccccct	ttngtgcctt	anagngnagc	480
gtgtccnanc	cnetcaacat	ganacgcgcc	agnccanccg	caattnggca	caatgtcgnc	540
gaacccccta	gggggantna	tncaaanccc	caggattgtc	cncncangaa	atcccnanc	600
cccnccttac	ccncttttgg	gacngtgacc	aantcccga	gtncacgtcc	ggccngnctc	660
ccccaccggt	nnccntgggg	gggtgaanct	cnngntcanc	cnngcagagn	ntcgnaagga	720
accggncctn	ggncgaanng	ancnntcnga	agngecnnt	cgtataaccc	cccctcncca	780
ncnancngnt	agntcccccc	cngggtncgg	aangg			815

<210> 25
 <211> 775
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(775)
 <223> n = A,T,C or G

ccgagatgtc	tcgtctccgtg	gccttagctg	tgctcgcgct	actctctctt	tctggcctgg	60
aggctatcca	gcgtactcca	aagattcagg	tttactcacg	tcattccagca	gagaatggaa	120
agtcaaattt	cctgaattgc	tatgtgtctg	gggttcatcc	atccgacatt	gaanttgcct	180
tactgaagaa	attgaaaag	attgaaaag	tggagcattc	agacttgtct	ttcagcaagg	240
actggtcttt	ctatctcntg	tactacactg	aattcacccc	cactgaaaaa	gatgagtatg	300
cctgccgtgt	gaaccatgtg	actttgtcac	agcccaagat	agttaagtgg	gatcgagaca	360
tgtaagcagn	cnncatggaa	gtttgaagat	gccgcatttg	gattggatga	attccaaatt	420
ctgcttgctt	gcntttta	antgatatgc	ntatacaccc	taccctttat	gncccaaat	480
tgtagggggt	acatnantgt	tcnctnngga	catgatcttc	ctttataant	ccnccnttcg	540
aattgcccgt	cncccngttn	ngaattgttc	cnnaaccacg	gttggctccc	ccaggtcncc	600
tcttacggaa	gggcctgggc	cnctttncaa	gggtggggga	accnaaaatt	tcncttntgc	660
ccncccncca	cnntcttgng	nnccncttt	ggaaaccttc	cnattcccc	tggcctcnna	720
nccttnncta	anaaaacttn	aaancgtngc	naaannttn	acttcccccc	ttacc	775

<210> 26
 <211> 820
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(820)
 <223> n = A,T,C or G

anattantac	agtgtaatct	tttcccagag	gtgtgtanag	ggaacggggc	ctagaggcat	60
cccanagata	ncttatanca	acagtgcctt	gaccaagagc	tgctgggcac	atttcctgca	120
gaaaagggtg	cgggtcccat	cactcctcct	ctcccatagc	catcccagag	gggtgagtag	180
ccatcangcc	ttcggtggga	gggagtcang	gaaacaacan	accacagagc	anacagacca	240
ntgatgacca	tgggcgggag	cgagcctctt	ccctgnaccg	gggtggcana	nganagccta	300
nctgaggggt	cacactataa	acgttaacga	ccnagatnan	cacctgcctc	aagtgcaccc	360
ttcctacctg	acnaccagng	accnnnaact	gcngcctggg	gacagcnctg	ggancagcta	420
acnnagcact	cacctgcccc	cccatggcgc	tnccgntccc	tggtcctgnc	aagggaagct	480
ccctgttgga	attncgggga	naccaaggga	nccccctcct	ccanctgtga	aggaaaaann	540
gatggaattt	tncccttcgc	gcenntcccc	tcttcttcta	cacgccccct	nnctactctc	600
tccctctntt	ntcctgncnc	acttttnacc	ccnnnatctc	ccttnattga	tcggannctn	660

ganattccac tnnccctnc cntcnatcng naanacnaaa nactntctna cccnggggat 720
 gggnnccctog ntcacccctct ctttttctct accnccnntt ctttgcctct ccttngatca
 780tccaacntc gntggccntn cccccccnnn tcctttncce
 820

<210> 27
 <211> 818
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(818)
 <223> n = A,T,C or G

<400> 27
 tctgggtgat ggcctcttcc tcctcagga cctctgactg ctctgggcca aagaatctct 60
 tgtttcttct ccgagcccca ggcagcgggtg attcagccct gcccaacctg attctgatga 120
 ctgcggatgc tgtgacggac ccaaggggca aatagggtcc cagggtccag ggaggggccc 180
 ctgctgagca cttccgcccc tcaccctgcc cagccctgc catgagctct gggctgggtc 240
 tccgctcca gggttctgct cttccangca ngccancaag tggcgtggg ccacactggc 300
 ttcttctgc cccntccctg gctctganc tctgtcttcc tgtcctgtgc angcnccttg 360
 gatctcagtt tccctcctc annaactct gtttctgann tcttcantta actntgantt 420
 tatnaccnan tggnetgtnc tgtcnnactt taatgggccc gaccggctaa tccctccctc 480
 nctcccttcc anttcnnnna accngcttnc cntctctcc ccntancccg ccngggaanc 540
 ctcttttgc ctnaccangg gccnnnaccg cccntnnctn ggggggcnng gtnnctnnc 600
 ctgntnccc cnetcncnt tncctcgtcc cnnccnccn nngcannttc nngtcccnn 660
 tnnctcttcn ngntcgnaa ngntcncntn tnnnnngcn ngntnntcn tccctctcnc 720
 cnnntgnang tntttnnnnc ncngncccc nnnccnnnn nggnntnnn tctnccngc 780
 cccncccc ngnattaagg cctccnntct ccggccnc 818

<210> 28
 <211> 731
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(731)
 <223> n = A,T,C or G

<400> 28
 aggaagggcg gaggatatt gtangggatt gagggatagg agnataangg gggaggtgtg 60
 tccaacatg anggtgnngt tctctttga angaggttg ngttttann ccnggtgggt 120
 gattnaaccc cattgtatgg agnnaaagg ttttagggat ttttcggctc ttatcagtat 180
 ntanattcct gtnaatcgga aaatnatntt tcnnccggaa aatnttgctc ccatccgnaa 240
 attnctcccg gtagtgcat nttnggggn cngccangtt tcccaggctg ctanaatcgt 300
 actaaagntt naagtgggan tncaaatgaa aacctnnccac agagnatccn taccgactg 360
 tnnntnccct tcgccctntg actctgcnn agcccaatac ccnngnngnat gtcnccnng 420
 nnnngcncnc tgaaannnnc tcgnggctnn gancatcang gggtttcgca tcaaaagcnn 480
 cgtttcncat naaggcactt tngcctcatc caaccnctng ccctcnncca tttngccgtc 540
 nggttcncc acgctnntng cncctnnntn ganattttnc ccgcctnggg naancctcct 600
 gnaatgggta gggncctntc ttttnaccnn gnggtntact aatcnnctnc acgctnctt 660
 tctnacccc ccccttttt caatcccanc ggcnaatggg gtctcccnn cgangggggg 720
 nnnccannc c 731

<210> 29
 <211> 822
 <212> DNA
 <213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(822)
 <223> n = A,T,C or G

<400> 29
 actagtccag tgtgggtggaa ttccattgtg ttgggggnenc ttctatgant antnttagat 60
 cgctcanacc tcacancctc ccnacnangc ctataangaa nannaataga nctgtncnnt 120
 atntntacnc tcatanncct cnnnacccac tccctcttaa cccntactgt gcctatngcn 180
 tnnctantct ntgccgcctn cnanccaccn gtggggccnac cncnngnatt ctcnatctcc 240
 tcnccatntn gcctananta ngtncatacc ctatacctac nccaatgcta nnnctaancn 300
 tccatnantt annntaacta ccactgacnt ngactttcnc atnancctct aatttgaatc 360
 tactctgact cccacngcct annnattagc ancntcccc nacnatntct caaccaaate 420
 ntcaacaacc tatctantctg ttcnccaacc nttncctccg atccccnnac aacccccctc 480
 ccaaataccc nccacctgac ncctaaccn caccatcccc gcaagccnan ggncatttan 540
 ccactggaat cacnatngga naaaaaaaaaa ccnaactctc tancncnnat ctccctaana 600
 aatnctcctn naatttactn ncantnccat caanccccacn tgaaacnnaa cccctgtttt 660
 tanatccctt ctttcgaaaa ccnacccttt annncccaac ctttngggcc cccccnctnc 720
 ccnaatgaag gncncccaat cnangaaacg nccntgaaaa ancnaaggcna anannntccg 780
 canatcctat cccttanttn ggggnccctt ncccnngggc cc 822

<210> 30
 <211> 787
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(787)
 <223> n = A,T,C or G

<400> 30
 cggccgcctg ctctggcaca tgcctcctga atggcatcaa aagtgatgga ctgcccattg 60
 ctagagaaga ccttctctcc tactgtcatt atggagccct gcagactgag ggctccccctt 120
 gtctgcagga tttgatgtct gaagtcgtgg agtgtggctt ggagctcctc atctacatna 180
 gctggaagcc ctggagggcc tctctcgcca gcctccccct tctctccacg ctctccangg 240
 acaccagggg ctccaggcag cccattattc ccagnangac atgggtgttc tccacgcgga 300
 cccatggggc ctgnaaggcc aggggtctcct ttgacaccat ctctcccgtc ctgcctggca 360
 ggccgtggga tccactantt ctanaacggn cgccaccncg gtggggagctc cagcttttgt 420
 tcccnttaat gaaggttaat tgcncgcttg gcgtaatcat nggtcanaac tntttcctgt 480
 gtgaaaattgt ttntcccctc ncnattccnc ncnacatacn aaccgggaan cataaagtgt 540
 taaagcctgg gggtngcctn nngaataaac tnaactcaat taattgcgtt ggctcatggc 600
 ccgctttccn ttcnngaaaa ctgtcntccc ctgcnttntt gaatcgggca cccccnggg 660
 aaaagcggtt tgcnttttng ggggntcctt ccncttcccc cctcnctaan ccctncgcct 720
 cggtcgttnc nggtngcggg gaangggnat nnnctccnc naagggggng agnnngntat 780
 ccccaaa 787

<210> 31
 <211> 799
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(799)
 <223> n = A,T,C or G

<400> 31
 tttttttttt tttttttggc gatgctactg ttttaattgca ggaggtgggg gtgtgtgtac 60
 catgtaccag ggctattaga agcaagaagg aaggaggagg ggcagagcgc cctgctgagc 120
 aacaaaggac tcctgcagcc ttctctgtct gtctcttggc gcaggcacat ggggaggcct 180
 cccgcagggt gggggccacc agtccagggg tgggagcact acanggggtg ggagtgggtg 240
 gtggctggtn cnaatggcct gncacanatc cctacgattc ttgacacctg gatttcacca 300


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ggggaccttc tgttctccca nggnaacttc ntnnatctcn aaagaacaca actgtttctt 360
cngcanttct ggctgttcat ggaaagcaca ggtgtccnat ttnggctggg acttggtaca 420
tatggttccg gccacactct cccntcnaaa aagtaattca ccccccccn ccntctnttg 480
cctgggccct taantaccca caccggaact canttanta ttcatcttng gntgggcttg 540
ntnatcnccn cctgaangcg ccaagttgaa aggccacgcc gtncnccnctc cccatagnan 600
nttttnnctn canctaatac cccccnnggc aacnatccaa tcccccccn tgggggcccc 660
agcccanggc ccccgntctg ggnnnccnng cncgnantcc ccaggntctc ccantcngnc 720
ccnnngcncc cccgcacgca gaacanaagg ntngagccnc cgcannnnnn nggtnnncac 780
ctcgcccccc ccnncgnng

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<210> 32
<211> 789
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(789)
<223> n = A,T,C or G

```

```

<400> 32
tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 60
tttttccnag ggcaggttta ttgacaacct cncgggacac aancaggctg gggacaggac 120
ggcaacaggc tccggcgccg gcggcgccgc ccctacctgc ggtaccaaata ntgcagcctc 180
cgctcccgtt tgatnttctt ctgcagctgc aggatgccnt aaaacagggc ctgcggccntn 240
ggtgggcacc ctgggatttn aatttccacg ggcacaatgc ggtcgcancc cctcaccacc 300
nattaggaat agtggtnnta cccnccnccg ttggcncact ccccntggaa accacttntc 360
gcggctcccg catctggtct taaaccttgc aaacnctggg gccctctttt tggttantnt 420
nccngccaca atcatnactc agactggcnc gggtggcccc caaaaaanctn ccccaaaacc 480
ggncatgtc ttnnccgggt tgetgcnatn tncatcacct cccgggcnca ncaggnaaac 540
ccaaaagttc ttgnggccn caaaaaanct cccgggggnc ccagtttcaa caaagtcac 600
ccccttggcc cccaaatcct cccccgntt nctgggtttg ggaaccacg cctctnnctt 660
tggngggcaa gntggntccc ccttcgggcc cccggtgggc ccnctctaa ngaaaacncc 720
ntcctnnnca ccatcccccc nngnnacgnc tancaangna tccctttttt tanaaacggg 780
cccccnng

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<210> 33
<211> 793
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(793)
<223> n = A,T,C or G

```

```

<400> 33
gacagaacat gttggatggt ggagcacctt tctatacgac ttacaggaca gcagatgggg 60
aattcatggc tgttgagca atanaacccc agttctacga gctgctgac aaaggacttg 120
gactaaagtc tgatgaactt cccaatcaga tgagcatgga tgattggcca gaaatgaana 180
agaagtttgc agatgtattt gcaaagaaga cgaaggcaga gtggtgtcaa atctttgacg 240
gcacagatgc ctgtgtgact ccggttctga cttttgagga ggttgttcat catgatcaca 300
acaangaacg gggctcgttt atcaccantg aggagcagga cgtgagcccc cgccctgcac 360
ctctgctggt aaacacccca gccatccctt ctttcaaaag ggatccacta cttctagagc 420
ggncgccacc gcggtggagc tccagctttt gtcccttta gtgagggtta attgcgcgct 480
tggcgtaatc atggtcatan ctgtttctg tgtgaaattg ttatccgctc acaattccac 540
acaacatacg anccggaagc atnaaatttt aaagcctggn ggtngcctaa tgantgaact 600
nactcacatt aattggcttt gcgctcactg cccgctttcc agtccggaaa acctgtcctt 660
gccagctgcc nttaatgaat cnggccaccc cccggggaaa aggcngtttg cttnttgggg 720
cgcncttccc gctttctcgc ttctgaant ccttcccccc ggtctttcgg cttgcggcna 780
acggtatcna cct

```

15

<210> 34
 <211> 756
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(756)
 <223> n = A,T,C or G

<400> 34
 gccgcgaccg gcatgtacga gcaactcaag ggcgagtggga accgtaaaag ccccaatctt 60
 ancaagtgcg gggaanagct gggtcgactc aagctagttc ttctggagct caacttcttg 120
 ccaaccacag ggaccaagct gaccaaacag cagctaattc tggcccgtga catactggag 180
 atcggggccc aatggagcat cctacgcaan gacatccctt ccttcgagcg ctacatggcc 240
 cagctcaaat gctactactt tgattacaan gagcagctcc ccgagtcagc ctatatgcac 300
 cagctcttgg gectcaacct cctcttctcg ctgtcccaga accgggtggc tgantnccac 360
 acgganttgg ancggtgcc tgcccanga catacanacc aatgtctaca tcnaccacca 420
 gtgtcctgga gcaatactga tgganggcag ctaccncaaa gtnttctctg ccnagggtta 480
 catccccgcg cgagagctac accttcttca ttgacatcct gctcgacact atcagggatg 540
 aaaatcgcnng ggttgctcca gaaaggctnc aanaanatcc ttttctnctga aggcccccgg 600
 atnctnctagt nctagaatcg gcccgccatc gcggtgganc ctccaacctt tcgttnccct 660
 ttactgaggg ttnattgccg cccttggcgt tatcatggtc acnccngttn cctgtgttga 720
 aattnttaac cccccacaat tccacgcna cattng 756

<210> 35
 <211> 834
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(834)
 <223> n = A,T,C or G

<400> 35
 ggggatctct anactnacct gnatgcatgg ttgtcgggtg ggtcgctgtc gatgaanatg 60
 aacaggatct tgcccttgaa gctctcgctc gctgtnttta agttgctcag tctgccgtca 120
 tagtcagaca cncctctggg caaaaaacan caggatntga gtcttgattt cacctccaat 180
 aatcttcnng gctgtctgct cggtgaactc gatgacnang ggcagctggg tgtgtntgat 240
 aaantccanc angttctcct tggtagctc cccttcaaag ttgttccggc cttcatcaaa 300
 cttctnnaan angannancc canctttgtc gagctggnat ttgganaaca cgtcactgtt 360
 ggaaactgat cccaaatggg atgtcatcca tcgcctctgc tgcctgcaaa aaacttgctt 420
 ggcncaaatc cgactcccn tcttgaaag aagccnatca cacccectc cctggactcc 480
 nncaangact ctncgcgtnc cccntccnng cagggttggg ggcannccgg gccntgcgc 540
 ttcttcagcc agttcaacn ntcatcagc ccctctgcca gctgtntat tcttggggg 600
 ggaanccgtc tctcccttcc tgaannaact ttgaccgtng gaatagccgc gntcncnt 660
 acntnctggg ccgggttcaa antccctccn ttgnenntcn cctcgggcca ttctggattt 720
 nccnaacttt tctcttcccc cncctcncgg ngtttggntt tttcatnggg ccccaactct 780
 gctnttggcc antccctggg gggcntntan cncctcctnt ggtcccntng ggcc 834

<210> 36
 <211> 814
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(814)
 <223> n = A,T,C or G

<400> 36

cggnccgcttt	ccngccgcgc	cccgtttcca	tgacnaaggc	tccttcang	ttaaatacnn	60
cctagnaaac	attaatgggt	tgctctacta	atacatcata	cnaaccagta	agcctgcca	120
naacgccaac	tcaggccatt	cctaccaaag	gaagaaaggc	tggtctctcc	acccctgta	180
ggaaaggcct	gccttgtaag	acaccacaat	ncggctgaat	ctnaagtctt	gtgttttact	240
aatggaaaaa	aaaaataaac	aanaggtttt	gttctcatgg	ctgcccaccg	cagcctggca	300
ctaaaacanc	ccagcgctca	cttctgcttg	ganaaatatt	ctttgctctt	ttggacatca	360
ggcttgatgg	tatcactgcc	acntttccac	ccagctgggc	ncctttcccc	catntttgtc	420
antganctgg	aaggcctgaa	nccttagctc	caaaagtctc	ngcccacaag	accggccacc	480
aggggangtc	ntttncagtg	gatctgcaa	anantaccn	tatcatcnnt	gaataaaaag	540
gcccctgaac	ganatgcttc	cancancctt	taagacccat	aatcctngaa	ccatgggtgc	600
cttccggtct	gatccnaaag	gaatgttcct	gggtcccant	ccctcctttg	ttnccttacgt	660
tgtnttgac	ccntgctngn	atnaccaan	tgantcccc	ngaagcacc	tnccctggc	720
atttganttt	cntaaattct	ctgccctacn	netgaaagca	cnattccctn	ggcnccnaan	780
ggngaactca	agaaggtctn	ngaaaaacca	cncn			814

<210> 37
 <211> 760
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(760)
 <223> n = A,T,C or G

<400> 37						
gcattgctgct	cttcctcaaa	gttggttcttg	ttgccataac	aaccaccata	ggtaaagcgg	60
gcgcagtgtt	cgctgaaggg	gttgtagtac	cagcgcgggga	tgctctcctt	gcagagtcct	120
gtgtctggca	gggtccagca	atgccctttg	tacttgggga	aatggatgcy	ctggagctcg	180
tcnaanccac	tcgtgtattt	ttcacangca	gcctcctccg	aagctccgg	gcagttgggg	240
gtgtcgtcac	actccactaa	actgtcgatn	cancagccca	ttgtctgcagc	ggaactgggt	300
gggctgacag	gtgccagaac	acactggatn	ggcctttcca	tggaagggcc	tgggggaaat	360
cncctnancc	caaactgcct	ctcaaaggcc	accttgacac	ccccgacagg	ctagaaatgc	420
actcttcttc	ccaaaggtag	ttgttcttgt	tgcccaagca	ncctccanca	aaccaaana	480
ttgcaaaaatc	tgctccgtgg	gggtcatnnn	taccanggtt	ggggaaanaa	acccggcngn	540
ganccnccct	gtttgaatgc	naaggnaata	atcctcctgt	cttgcttggg	tggaanagca	600
caattgaact	gttaacnttg	ggccgngttc	cncctnggtg	gtctgaaact	aatcacctgc	660
actggaaaaa	ggtangtgcc	ttccttgaat	tcccaaantt	cccctngntt	tggtgnnttt	720
ctcctctncc	ctaaaaatcg	tnntcccccc	centanggcg			760

<210> 38
 <211> 724
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(724)
 <223> n = A,T,C or G

<400> 38						
tttttttttt	tttttttttt	tttttttttt	tttttaaaaa	ccccctccat	tgaatgaaaa	60
cttcnnaaat	tgtccaaccc	cctcnnccaa	atnnccattt	ccgggggggg	gttccaaacc	120
caaattaatt	ttgganttta	aattaaatnt	tnattngggg	anaaanccaa	atgtnaagaa	180
aatttaaccc	attatnaact	taaatncctn	gaaacccntg	gnttccaaaa	atttttaacc	240
cttaaatccc	tccgaaattg	ntaanggaaa	accaaattcn	cctaaggctn	tttgaaggtt	300
ngatttaaac	ccccttnant	tnntttnacc	cnngnctnaa	ntatttngnt	tccggtgttt	360
tcctnttaan	cntnggtaac	tcccgnfaat	gaannnccct	aanccaatta	aaccgaattt	420
tttttgaatt	ggaaattccn	ngggaattna	ccgggggttt	tccnttttgg	gggccatncc	480
cccnctttcg	gggtttgggn	ntaggttgaa	tttttnnang	ncccaaaaaa	nccccaana	540
aaaaaactcc	caagnnttaa	ttngaantnc	ccccttccca	ggccttttgg	gaaaggnggg	600
ttnttggggg	cnngggantt	cnttcccccn	tnccncccc	ccccccnggt	aaanggttat	660

ngnnttttgggt ttttgggccc cttnangggac cttccggatn gaaattaaat ccccgggncg 720
gccg 724

<210> 39
<211> 751
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(751)
<223> n = A,T,C or G

<400> 39
tttttttttt tttttctttg ctcacattta atttttattt tgattttttt taatgctgca 60
caacacaata tttatttcat ttgtttcttt tatttcattt tatttgtttg ctgctgctgt 120
tttattttatt tttactgaaa gtgagaggga actttttgtg ccttttttcc tttttctgta 180
ggccgcctta agctttctaa atttggaaac tctaagcaag ctgaanggaa aaggggggtt 240
cgcaaaaatca ctcgggggaa nggaaagggt gctttgttaa tcatgcccta tgggtgggtga 300
ttaactgctt gtacaattac ntttactttt taattaattg tgctnaangc ttttaattana 360
cttgggggtt ccttccccc accaaccnccn ctgacaaaaa gtgccngccc tcaaatnatg 420
tcccgcnnt ctttgaaca cacngcngaa ngttctcatt ntcccnccnc caggtnaaaa 480
tgaagggtta ccatntttta cncacctcc acntggcnnn gcctgaatcc tcnaaaancn 540
ccctcaannc aattntnng ccccggtcnc gcntnngtcc cncggggct cgggaantn 600
caccnccnga annnntnnc naacnaaatt ccgaaaatat tccnntcnc tcaattcccc 660
cnnagactnt cctcnnncn cncaattttc tttntntcac gaacncgnnc cnnaaatgn 720
nnnnncctc cncnngtcn naatcnccan c 751

<210> 40
<211> 753
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(753)
<223> n = A,T,C or G

<400> 40
gtggtatttt ctgtaagatc aggtgttcct cctcgtagg ttttagaggaa acaccctcat 60
agatgaaaac ccccccgaga cagcagcact gcaactgcc aagcagccgg gtaggagggg 120
cgccctatgc acagctgggc ccttgagaca gcagggttc gatgtcaggc tcgatgtcaa 180
tggctctgaa gcggcgctg tacctgcgta ggggcacacc gtcaggggcc accaggaact 240
tctcaaagtt ccaggcaacn tcgttgcgac acaccggaga ccaggtgatn agcttggggt 300
cggtcataa cgggtggcg tcgtcgtgg gagctggcag ggcctccgc aggaaggcna 360
ataaaagggt gcggcccgca ccgttcantc cgcacttctc naanaccatg angttgggct 420
cnaaccacc accannccgg acttccttga nggaattccc aaatctcttc gntcttgggc 480
ttctnctgat gccctantc gttgccnngn atgccaanca nccccancc cgggggtcct 540
aaanaccn cctctcntt tcatctgggt tntntcccc ggacnctgg tctctcaag 600
gganccata tctnaccan tactcaccnt nccccccnt gnnaccanc cttctanngn 660
ttccncccg ncctctggcc cntcaaan gcttnacna cctgggtctg cttcccccc 720
tnccctatct gnaccnccn tttgtctcan tnt 753

<210> 41
<211> 341
<212> DNA
<213> Homo sapien

<400> 41
actatatcca tcacaacaga catgcttcat cccatagact tcttgacata gcttcaaatg 60
agtgaacca tccttgattt atatacatat atgttctcag tattttggga gcctttccac 120
ttctttaaac cttgttcatt atgaacactg aaaataggaa tttgtgaaga gttaaaaagt 180

tatagcttgt	ttacgtagta	agtttttgaa	gtctacattc	aatccagaca	cttagttgag	240
tggtaaactg	tgatttttaa	aaaatatcat	ttgagaatat	tctttcagag	gtattttcat	300
ttttactttt	tgattaattg	tgttttatat	attagggtag	t		341

<210> 42
 <211> 101
 <212> DNA
 <213> Homo sapien

<400> 42						
acttactgaa	tttagttctg	tgctcttcct	tatttagtgt	tgtatcataa	atactttgat	60
gtttcaaaca	ttctaaataa	ataattttca	gtggcttcat	a		101

<210> 43
 <211> 305
 <212> DNA
 <213> Homo sapien

<400> 43						
acatctttgt	tacagtctaa	gatgtgttct	taaatcacca	ttccttcctg	gtcctcaccc	60
tccaggttgg	tctcacactg	taattagagc	tattgaggag	tctttacagc	aaattaagat	120
tcagatgcct	tgctaagtct	agagttctag	agttatgttt	cagaaagtct	aagaaaccca	180
cctcttgaga	ggtcagtaaa	gaggacttaa	tatttcatat	ctacaaaatg	accacaggat	240
tggtacacaga	acgagagtta	tcctggataa	ctcagagctg	agtacctgcc	cggggggccgc	300
tcgaa						305

<210> 44
 <211> 852
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(852)
 <223> n = A,T,C or G

<400> 44						
acataaatat	cagagaaaag	tagtctttga	aatatttacg	tccaggagtt	ctttgtttct	60
gattattttg	tgtgtgtttt	ggtttgtgtc	caaagtattg	gcagcttcag	ttttcatttt	120
ctctccatcc	tcgggcattc	ttcccaaatt	tatataccag	tcttcgtcca	tcacacgcct	180
ccagaatttc	tctttttag	taatatctca	tagctcggct	gagcttttca	taggtcatgc	240
tgctgtgtgt	cttcttttta	ccccatagct	gagccactgc	ctctgatttc	aagaacctga	300
agacgccctc	agatcggctc	tcccatttta	ttaatcctgg	gttcttgtct	gggttcaaga	360
ggatgtcgcg	gatgaattcc	cataagttag	tcctctcctg	gttgtgcttt	ttgggtgtgc	420
acttggcagg	gggtctctgc	tcctttttca	tatcaggtga	ctctgcaaca	ggaaggtgac	480
tggtggttgt	catggagatc	tgagcccggc	agaaagtgtt	gctgtccaac	aaatctactg	540
tgctaccata	gttggtgtca	tataaatagt	tctngtcttt	ccaggtgttc	atgatggaag	600
gctcagtttg	ttcagtcttg	acaatgacat	tgtgtgtgga	ctggaacagg	tcactactgc	660
actggccggt	ccacttcaga	tgctgcaagt	tgctgtagag	gagntgcccc	gccgtccctg	720
ccgcccggtg	gaactcctgc	aaactcatgc	tgcaaagggt	ctcgccgttg	atgtcgaaat	780
cntggaaagg	gatacaattg	gcattccagct	ggttggtgtc	caggaggtga	tgtagccact	840
cccacacctg	gt					852

<210> 45
 <211> 234
 <212> DNA
 <213> Homo sapien

<400> 45						
acaacagacc	cttgctcgtc	aacgacctca	tgctcatcaa	gttggacgaa	tccgtgtccg	60
agtctgacac	catccggagc	atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	120
gcctcgtttc	tggtctgggt	ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	180

tgaacgtgtc ggtggtgtct gaggaggtct gcagtaagct ctatgaccgc ctgt 234

<210> 46
 <211> 590
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(590)
 <223> n = A,T,C or G

<400> 46
 actttttatt taaatgttta taaggcagat ctatgagaat gatagaaaac atggtgtgta 60
 atttgatagc aatatttttg agattacaga gtttttagta ttaccaatta cacagttaaa 120
 aagaagataa tatattccaa gcanatacaa aatatctaata gaaagatcaa ggcaggaaaa 180
 tgantataac taattgacaa tggaaaatca attttaatgt gaattgcaca ttatccttta 240
 aaagctttca aaanaanaaa ttattgcagt ctanttaatt caaacagtgat taaatggtat 300
 caggataaan aactgaaggg canaaagaat taattttcac ttcattgtaac ncaccanatt 360
 ttacaatggc ttaaatgcan ggaaaaagca gtggaagtag ggaagtantc aaggtctttc 420
 tggctctctaa tctgccttac tctttgggtg tggctttgat cctctggaga cagctgccag 480
 ggctcctgtt atatccacaa tccagcagc aagatgaagg gatgaaaaag gacacatgct 540
 gccttccttt gaggagactt catctcactg gccaacactc agtcacatgt 590

<210> 47
 <211> 774
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(774)
 <223> n = A,T,C or G

<400> 47
 acaagggggc ataatgaagg agtgggggana gatttttaag aaggaaaaaa aacgaggccc 60
 tgaacagaat tttcctgnac aacggggcctt caaaataatt ttcttgggga ggttcaagac 120
 gcttcactgc ttgaaactta aatggatgtg ggacanaatt ttctgtaatg accctgaggg 180
 cattacagac gggactctgg gaggaaggat aaacagaaag gggacaaagg ctaatcccaa 240
 aacatcaaag aaaggaaggt ggcgtcatal ctcccagcct acacagttct ccagggtctt 300
 cctcatccct ggaggacgac agtggaggaa caactgacca tgtccccagg ctctgtgtg 360
 ctggctcctg gtcttcagcc ccagctctg gaagcccacc ctctgctgat cctgcgtggc 420
 ccacactcct tgaacacaca tccccaggtt atattcctgg acatggctga acctcctatt 480
 cctacttccg agatgccttg ctccctgcag cctgtcaaaa tcccactcac cctccaaacc 540
 acggcatggg aagcctttct gacttgcttg attactccag catcttgga caatccctga 600
 ttccccactc cttagaggca agatagggtg gttaagagta gggctggacc acttgagacc 660
 aggtgctgg cttcaaattn tggctcattt acgagctatg ggaccttggg caagtnatct 720
 tcacttctat gggcntcatt ttgttctacc tgcaaaatgg gggataataa tagt 774

<210> 48
 <211> 124
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(124)
 <223> n = A,T,C or G

<400> 48
 canaaattga aattttataa aaaggcattt ttctcttata tccataaaat gatataattt 60
 ttgcaantat anaaatgtgt cataaattat aatgttcctt aattacagct caacgcaact 120

tggt 124

<210> 49
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 49
 gccgatgcta ctattttatt gcaggaggtg ggggtgtttt tattattctc tcaacagctt 60
 tgtggctaca ggtggtgtct gactgcatna aaaanttttt tacgggtgat tgcaaaaatt 120
 ttagggcacc catatcccaa gcantgt 147

<210> 50
 <211> 107
 <212> DNA
 <213> Homo sapien

<400> 50
 acattaaatt aataaaagga ctgttggggt tctgctaaaa cacatggctt gatatatgtc 60
 atggtttgag gttaggagga gttaggcata tgttttggga gaggggt 107

<210> 51
 <211> 204
 <212> DNA
 <213> Homo sapien

<400> 51
 gtcctaggaa gtctagggga cacacgactc tgggggtcacg gggccgacac acttgcacgg 60
 cgggaaggaa aggcagagaa gtgacaccgt cagggggaaa tgacagaaag gaaaatcaag 120
 gccttgcaag gtcagaaagg ggactcaggg cttccaccac agccctgccc cacttggcca 180
 cctccctttt gggaccagca atgt 204

<210> 52
 <211> 491
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(491)
 <223> n = A,T,C or G

<400> 52
 acaaagataa catttatctt ataacaaaaa tttgatagtt ttaaaggtta gtattgtgta 60
 gggatatttc caaaaagacta aagagataac tcaggtaaaa agttagaaat gtataaaaca 120
 ccatcagaca ggttttttaa aaacaacata ttacaaaatt agacaatcat ccttaaaaaa 180
 aaaacttctt gtatcaattt cttttgttca aaatgactga ctttaantatt tttaaatatt 240
 tcanaaacac ttcctcaaaa attttcaana tggtagcttt canatgtnc ctcagtccca 300
 atgttgctca gataaataaa tctcgtgaga acttaccacc caccacaagc tttctggggc 360
 atgcaacagt gtcttttctt tnccttttct tttttttttt ttacaggcac agaaactcat 420
 caattttatt tggataacaa aggggtctcca aatttatattg aaaaataaat ccaagttaat 480
 atcactcttg t 491

<210> 53
 <211> 484
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(484)
 <223> n = A,T,C or G

<400> 53
 acataattta gcagggctaa ttaccataag atgctattta ttaanaggtn tatgatctga 60
 gtattaacag ttgctgaagt ttggtatttt tatgcagcat tttctttttg ctttgataac 120
 actacagaac ccttaaggac actgaaaatt agtaagtataa gttcagaaac attagctgct 180
 caatcaaatac tctacataac actatagtaa ttaaaacggt aaaaaaaagt gttgaaatct 240
 gcactagtat anaccgctcc tgtcaggata anactgcttt ggaacagaaa gggaaaaanc 300
 agctttgant tttttgtgct tgatangagg aaaggctgaa ttaccttggt gcctctccct 360
 aatgattggc aggtcnggta aatnccaaaa catattccaa ctcaacactt cttttccncg 420
 tancttgant ctgtgtattc caggancagg cggatggaat gggccagccc ncggatgttc 480
 cant 484

<210> 54
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 54
 actaaacctc gtgcttgtga actccataca gaaaacggtg ccatccctga acacggctgg 60
 ccaactggga tactgctgac aaccgcaaca acaaaaacac aaatccttgg cactggctag 120
 tctatgtcct ctcaagtgcc tttttgtttg t 151

<210> 55
 <211> 91
 <212> DNA
 <213> Homo sapien

<400> 55
 acctggcttg tctccgggtg gttcccggtg cccccacgg tccccagAAC ggacactttc 60
 gccctccagt ggatactcga gccaaagtgg t 91

<210> 56
 <211> 133
 <212> DNA
 <213> Homo sapien

<400> 56
 ggaggatgtg cgttggttat atacaaatat gtcattttat gtaagggaact tgagtatact 60
 tggatttttg gtatctgtgg gttgggggga cggctcagga accaataccc catggatacc 120
 aagggacaac tgt 133

<210> 57
 <211> 147
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(147)
 <223> n = A,T,C or G

<400> 57
 actctggaga acctgagccg ctgctccgcc tctgggatga ggtgatgcan gcngtggcgc 60
 gactgggagc tgagcccttc cttttgcgcc tgcctcagag gattgttgcc gacntgcana 120
 tctcantggg ctggatncat gcagggt 147

<210> 58

<211> 198
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(198)
 <223> n = A,T,C or G

<400> 58
 acagggatat aggtttnaag ttattgtnat tgtaaaatac attgaatttt ctgtatactc 60
 tgattacata catttatcct ttaaaaaaga tgtaaatcctt aatttttatg ccatctatta 120
 atttaccaat gagttacctt gtaaatgaga agtcatgata gcactgaatt ttaactagtt 180
 ttgacttcta agtttggt 198

<210> 59
 <211> 330
 <212> DNA
 <213> Homo sapien

<400> 59
 acaacaaatg gggtgtgagg aagtcttatac agcaaaactg gtgatggcta ctgaaaagat 60
 ccattgaaaa ttatcattaa tgatttttaa tgacaagtta tcaaaaactc actcaatttt 120
 cacctgtgct agcttgctaa aatgggagtt aactctagag caaatatagt atcttctgaa 180
 tacagtcaat aaatgacaaa gccagggcct acaggtggtt tccagacttt ccagaccag 240
 cagaagggaat ctattttatc acatggatct ccgtctgtgc tcaaaatacc taatgatatt 300
 tttcgtcttt attggacttc tttgaagagt 330

<210> 60
 <211> 175
 <212> DNA
 <213> Homo sapien

<400> 60
 accgtgggtg ccttctacat tcttgacggc tctttcacca acatctggtt ctacttcggc 60
 gtcgtgggct ccttcctctt catcctcatc cagctgggtc tgctcatcga ctttgcgac 120
 tcttggaacc agcgggtggct gggcaaggcc gaggagtgcg attcccgtgc ctggt 175

<210> 61
 <211> 154
 <212> DNA
 <213> Homo sapien

<400> 61
 accccacttt tctcctgtg agcagctctgg acttctcact gctacatgat gagggtgagt 60
 ggttggtgct cttcaacagt atcctcccct ttccggatct gctgagccgg acagcagtc 120
 tggactgcac agccccgggg ctccacattg ctgt 154

<210> 62
 <211> 30
 <212> DNA
 <213> Homo sapien

<400> 62
 cgctcgagcc ctatagtgag tcgtattaga 30

<210> 63
 <211> 89
 <212> DNA
 <213> Homo sapien

<400> 63

acaagtcatt tcagcaccct ttgctcttca aaactgacca tcttttatat ttaatgcttc 60
ctgtatgaat aaaaatgggt atgtcaagt 89

<210> 64
<211> 97
<212> DNA
<213> Homo sapien

<400> 64
accggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa ggttctgcag 60
aatcagtga tccaggattg gtccttggat ctgggggt 97

<210> 65
<211> 377
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(377)
<223> n = A,T,C or G

<400> 65
acaacaanaa ntcccttctt taggccactg atggaaacct ggaacccctt tttgatggca 60
gcatggcgctc ctaggccttg acacagcggc tgggggtttg gctntcccaa accgcacacc 120
ccaaccctgg tctaccaca nttctggcta tgggctgtct ctgccactga acatcagggt 180
tcggtcataa natgaaatcc caanggggac agaggctcagt agaggaagct caatgagaaa 240
ggtgctgttt gctcagccag aaaacagctg cctggcattc gccgctgaac tatgaacccg 300
tggggggtgaa ctacccccan gaggaatcat gcctgggcga tgcaanggtg ccaacaggag 360
gggcgggagg agcatgt 377

<210> 66
<211> 305
<212> DNA
<213> Homo sapien

<400> 66
agcctttcc ctcagaattc agggaagaga ctgtcgctg ccttcctccg ttgttgctg 60
agaaccctg tgccccttc caccatatcc accctcgctc catctttgaa ctcaaacacg 120
aggaaactaac tgcaccctgg tctctcccc agtccccagt tcacctcca tccctcacct 180
tctccactc taagggatat caacactgcc cagcacaggg gccctgaatt tatgtggtt 240
ttatatattt ttttaataaga tgcactttat gtcatttttt aataaagtct gaagaattac 300
tgttt 305

<210> 67
<211> 385
<212> DNA
<213> Homo sapien

<400> 67
actacacaca ctccacttgc ccttgtgaga cactttgtcc cagcacttta ggaatgctga 60
ggtcgagacca gccacatctc atgtgcaaga ttgccagca gacatcaggt ctgagagttc 120
cccttttaaa aaaggggact tgcttaaaaa agaagtctag ccacgattgt gtagagcagc 180
tgtgtgtgctc tggagattca cttttgagag agttctcctc tgagacctga tcttttagag 240
ctgggcagtc ttgcacatga gatggggctg gtctgatctc agcactcctt agtctgcttg 300
cctctcccag ggccccagcc tggccacacc tgcttacagg gcactctcag atgcccatac 360
catagtttct gtgctagtgg accgt 385

<210> 68
<211> 73
<212> DNA
<213> Homo sapien

<400> 68
 acttaaccag atatattttt accccagatg gggatattct ttgtaaaaaa tgaaaataaa 60
 gtttttttaa tgg 73

<210> 69
 <211> 536
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(536)
 <223> n = A,T,C or G

<400> 69
 actagtccag tgtggtggaa ttccattgtg ttggggggctc tcaccctcct ctctgcagc 60
 tocagctttg tgctctgcct ctgaggagac catggcccag catctgagta ccctgctgct 120
 cctgctggcc accctagctg tggccctggc ctggagcccc aaggaggagg ataggataat 180
 cccgggtggc atctataacg cagacctcaa tgatgagtgg gtacagcgtg cccttcactt 240
 cgccatcagc gagtataaca aggccaccaa agatgactac tacagacgtc cgctgcgggt 300
 actaagagcc aggcaacaga ccgttggggg ggtgaattac ttcttcgacg tagagggtggg 360
 ccgaaccata tgtaccaagt cccagcccaa cttggacacc tgtgccttcc atgaacagcc 420
 agaactgcag aagaaacagt tgtgctcttt cgagatctac gaagtccctt ggggagaaca 480
 gaangtcctt gggtgaaatc caggtgtcaa gaaatcctan ggatctgttg ccaggc 536

<210> 70
 <211> 477
 <212> DNA
 <213> Homo sapien

<400> 70
 atgacccta acagggggccc tctcagccct cctaattgacc tccggcctag ccatgtgatt 60
 tcaattccac tccataacgc tcctcatact aggcctacta accaaccacac taaccatata 120
 ccaatgatgg cgcgatgtaa cagagaaaag cacataccaa ggccaccaca caccacctgt 180
 ccaaaaaggc cttcgatacg ggataatcct atttattacc tcagaagttt ttttcttcgc 240
 agggattttt ctgagccttt taccactcca gcttagcccc tacccccacaa ctaggagggc 300
 actggccccc aacaggcatc acccgcgtaa atcccctaga agtcccactc ctaaacacat 360
 ccgtattact cgcatacagg gtatcaatca cctgagctca ccatagtcta atagaaaaca 420
 accgaaacca aattattcaa agcactgctt attacaattt tactgggtct ctatttt 477

<210> 71
 <211> 533
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(533)
 <223> n = A,T,C or G

<400> 71
 agagctatag gtacagtgtg atctcagctt tgcaaacaca ttttctacat agatagtact 60
 aggtattaat agatatgtaa agaaagaaat cacaccatta ataatggtaa gattggttta 120
 tgtgatttta gtggtatttt tggcaccctt atatattgtt tccaaacttt cagcagtgat 180
 attattttcca taacttaaaa agtgagtttg aaaaagaaaa tctccagcaa gcatctcatt 240
 taaataaagg tttgtcatct ttaaaaatac agcaatatgt gactttttta aaaagctgtc 300
 aaataggtgt gaccctacta ataattatta gaaatacatt taaaaacatc gagtacctca 360
 agtcagtttg ccttgaaaaa tatcaaatat aactcttaga gaaatgtaca taaaagaatg 420
 cttcgtaatt ttggagtang aggttccttc ctcaattttg tattttttaa aagtacatgg 480
 taaaaaaaaa aattcacaac agtatataag gctgtaaaaat gaagaattct gcc 533

<210> 72

<211> 511
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(511)
 <223> n = A,T,C or G

<400> 72
 tattacggaa aaacacacca cataattcaa ctancaaaga anactgcttc agggcgtgta 60
 aaatgaaagg cttccaggca gttatctgat taaagaacac taaaagagg acaaggctaa 120
 aagccgcagg atgtctacac tatancaggc gctatttggg ttggctggag gagctgtgga 180
 aaacatggan agattggtgc tgganacgc cgtggctatt cctcattgtt attacanagt 240
 gaggttctct gtgtgcccac tggtttgaaa accgttctnc aataatgata gaatagtaca 300
 cacatgagaa ctgaaatggc ccaaaccag aaagaaagcc caactagatc ctcagaanac 360
 gcttctaggg acaataaccg atgaagaaa gatggcctcc ttgtgcccc gtctgttatg 420
 atttctctcc attgcagcna naaaccggtt cttctaagca aacncagggt atgatggcna 480
 aaatacaccc cctcttgaag naccnggagg a 511

<210> 73
 <211> 499
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(499)
 <223> n = A,T,C or G

<400> 73
 cagtgccagc actggtgccg gtaccagtac caataacagt gccagtgccg gtgccagcac 60
 cagtgtggc ttcagtgtg gtgccagcct gaccgccact ctcacatttg ggctcttcgc 120
 tggccttggg ggagctggtg ccagcaccag tggcagctct ggtgcctgtg gttcttccta 180
 caagtgaagt tttagatatt gttaatcctg ccagctcttc tcttcaagcc aggggtgcac 240
 ctcagaaacc tactcaacac agcactctag gcagccacta tcaatcaatt gaagttgaca 300
 ctctgcatta aatctatttg ccatcttctga aaaaaaaaa aaaaaaagg cggccgctcg 360
 antctagagg gcccgtttaa acccgctgat cagcctcgac tgtgccttct anttgccagc 420
 catctgtgtg ttgcccctcc cccgntgcct tccttgaccc tggaaagtgc cactcccact 480
 gtcctttcct aantaaaat 499

<210> 74
 <211> 537
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(537)
 <223> n = A,T,C or G

<400> 74
 tttcatagga gaacacactg aggagatact tgaagaattt ggattcagcc gcgaagagat 60
 ttatcagctt aactcagata aaatcattga agtaataaag gtaaaagcta gtctctaact 120
 tccaggccca cggctcaagt gaatttgaat actgcattta cagtgtagag taacacataa 180
 cattgtatgc atggaaacat ggaggaacag tattacagtg tctaccact ctaatcaaga 240
 aaagaattac agactctgat tctacagtga tgattgaatt ctaaaaatgg taatcattag 300
 ggcttttgat ttataanact ttgggtactt atactaaatt atggtagtta tactgccttc 360
 cagtttgctt gatataattg ttgatattaa gattcttgac ttatattttg aatgggttct 420
 actgaaaaan gaatgatata ttcttgaaga catcgatata catttattta cactcttgat 480
 tctacaatgt agaaaatgaa ggaaatgccc caaattgtat ggtgataaaa gtcccgt 537

<210> 75
 <211> 467
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(467)
 <223> n = A,T,C or G

<400> 75
 caaanacaat tgttcaaaag atgcaaatga tacactactg ctgcagctca caaacacctc 60
 tgcattattac acgtacctcc tcctgctcct caagtagtgt ggtctatatt gccatcatca 120
 cctgctgtct gcttagaaga acggctttct gctgcaangg agagaaatca taacagacgg 180
 tggcacaagg aggccatctt ttcctcatcg gttattgtcc ctagaagcgt cttctgagga 240
 tctagtggg ctttctttct gggtttgggc catttcantt ctcattgtgt tactattcta 300
 tcattattgt ataacggtt tcaaaccngt gggcacncag agaacctcac tctgtaataa 360
 caatgaggaa tagccacggt gatctccagc accaaatctc tccatgttnt tccagagctc 420
 ctccagccaa cccaaatagc cgctgctatn gtgtagaaca tccctgn 467

<210> 76
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 76
 aagctgacag cattcgggcc gagatgtctc gctccgtggc cttagctgtg ctgcgctac 60
 tctctctttc tggcctggag gctatccagc gtactccaaa gattcaggtt tactcacgct 120
 atccagcaga gaatggaaag tcaaatttcc tgaattgcta tgtgtctggg ttcatccat 180
 ccgacattga agttgactta ctgaagaatg gagagagaat tgaaaaagtg gagcattcag 240
 acttgtcttt cagcaaggac tggcttttct atctcttgta ctacactgaa ttcaccccca 300
 ctgaaaaaga tgagtatgcc tgccgtgtga accatgtgac tttgtcacag cccaagatng 360
 tttagtgagg taanacatg taagcagcan catgggaggt 400

<210> 77
 <211> 248
 <212> DNA
 <213> Homo sapien

<400> 77
 ctggagtgcc ttggtgtttc aagccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc cggcgggga tgcgaggctc ggagcaccct tgcccggctg tgattgctgc 120
 caggcactgt tcatctcagc ttttctgtcc ctttgtctcc ggcaagcgt tctgctgaaa 180
 gttcatatct ggagcctgat gtcttaacga ataaaggtcc catgctccac ccgaaaaaaa 240
 aaaaaaaa 248

<210> 78
 <211> 201
 <212> DNA
 <213> Homo sapien

<400> 78
 actagtccag tgtggtggaa ttccattgtg ttgggcccaa cacaatggct acctttaaca 60
 tcaccagac cccgcctgc ccgtgcccga cgctgtgtct aacgacagta tgatgcttac 120
 tctgtactc ggaaactatt tttatgtaat taatgtatgc tttcttgttt ataatgcct 180
 gatttaaaaa aaaaaaaaaa a 201

<210> 79
 <211> 552
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(552)
 <223> n = A,T,C or G

<400> 79
 tcctttttgtt aggtttttga gacaacccta gacctaaact gtgtcacaga cttctgaatg 60
 tttaggcagt gctagtaatt tcctcgtaat gattctgtta ttactttcct attctttatt 120
 cctctttctt ctgaagatta atgaagtga aaattgaggt ggataaatac aaaaaggtag 180
 tgtgatagta taagtatcta agtgcagatg aaagtgtgtt atatatatcc attcaaaatt 240
 atgcaagtta gtaattactc aggggttaact aaattacttt aatatgctgt tgaacctact 300
 ctgttccttg gctagaaaaa attataaaca ggactttgtt agtttgggaa gccaaattga 360
 taatattcta tgttctaaaa gttgggctat acataaanta tnaagaaata tggaatttta 420
 ttcccaggaa tatgggggtc atttatgaat antaccggg anagaagttt tgantnaaac 480
 cngttttgtt taatacgtta atatgtcctn aatnaacaag gcntgactta tttccaaaaa 540
 aaaaaaaaaa aa 552

<210> 80
 <211> 476
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 80
 acagggtatt gagatgctaa ggccccagag atcgtttgat ccaaccctct tattttcaga 60
 ggggaaaatg gggcctagaa gttacagagc atctagctgg tgcgctggca cccctggcct 120
 cacacagact cccgagtgc tgggactaca ggcacacagt cactgaagca ggccctgttt 180
 gcaattcacg ttgccacctc caacttaaac attcttcata tgtgatgtcc ttagtcacta 240
 aggttaaact ttcccacca gaaaaggcaa cttagataaa atcttagagt actttcatac 300
 tcttctaagt cctcttcag cctcactttg agtcctcctt gggggttgat aggaantntc 360
 tcttggttt ctcaataaaa tctctatcca tctcatgttt aatttggtac gcntaaaaat 420
 gctgaaaaaa ttaaaatgtt ctggtttcnc tttaaaaaaa aaaaaaaaaa aaaaaa 476

<210> 81
 <211> 232
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(232)
 <223> n = A,T,C or G

<400> 81
 ttttttttg tatgcntcn ctgtgnggtt attgttgctg ccaccctgga ggagcccagt 60
 ttcttctgta tctttctttt ctgggggagc ttcttggtc tgccctcca tcccagcct 120
 ctcacccca tcttgactt ttgctagggt tggaggcgt ttcttggtag cccctcagag 180
 actcagtcag cgggaataag tcctaggggt ggggggtgtg gcaagccggc ct 232

<210> 82
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 82
 aggcgggagc agaagctaaa gccaaagccc aagaagagtgc cagtggccag cactgggtgcc 60
 agtaccagta ccaataacat gccagtgccac cagtgggtggc ttcagtgtctg 120
 gtgccagcct gaccgccaact ctcacatttg ggctcttcgc tggccttggt ggagctgggtg 180
 ccagcaccag tggcagctct ggtgcctgtg gtttctccta caagtgagat tttagatatt 240
 gttaatcctg ccagtctttc tcttcaagcc aggggtgcac ctcagaaacc tactcaacac 300
 agcactctng gcagccacta tcaatcaatt gaagttgaca ctctgcatta aatctatttg 360
 ccatttcaaa aaaaaaaaaa aaa 480

<210> 83
 <211> 494
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(494)
 <223> n = A,T,C or G

<400> 83
 accgaattgg gaccgctggc ttataagcga tcatgtcctc cagtattacc tcaacgagca 60
 gggagatcga gtctatacgc tgaagaaatt tgaccgatg ggacaacaga cctgctcagc 120
 ccactctgct cggttctccc cagatgacaa atactctcga caccgaatca ccatcaagaa 180
 acgcttcaag gtgctcatga ccagcaacc gcgacctgtc ctctgagggt ccttaaaactg 240
 atgtcttttc tgccacctgt taccctctcg agactccgta accaaaactct tcggactgtg 300
 agccctgatg cctttttgcc agccatactc tttggcntcc agtctctcgt ggcgattgat 360
 tatgcttggtg tgaggcaatc atgggtggcat caccatnaa gggaacacat ttganttttt 420
 tttncatat ttttaattac naccagaata ntccagaata aatgaattga aaaactctta 480
 aaaaaaaaaa aaaa 494

<210> 84
 <211> 380
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(380)
 <223> n = A,T,C or G

<400> 84
 gctggtagcc tatggcgtgg ccacggangg gctcctgagg caggggacag tgacttccca 60
 agtatcctgc gccgcgtctt ctaccgtccc tacctgcaga tcttcgggca gattccccag 120
 gaggacatgg acgtggccct catggagcac agcaactgct cgtcggagcc cggcttctgg 180
 gcacaccctc ctggggccca ggcgggcacc tgcgtctccc agtatgccaa ctggctgggtg 240
 gtgctgtctc tcgtcatctt cctgctcgtg gccaacatcc tgcgtgtcac ttgctcattg 300
 ccatgttcag ttacacattc ggcaaagtac agggcaacag cnatctctac tgggaaggcc 360
 agcgtnccg cctcatccgg 480

<210> 85
 <211> 481
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(481)

<223> n = A,T,C or G

<400> 85

gagttagctc	ctccacaacc	ttgatgaggt	cgtctgcagt	ggcctctcgc	ttcataccgc	60
tnccatcgtc	atactgtagg	tttgccacca	cctcctgcat	cttggggcgc	ctaatatcca	120
ggaaactctc	aatcaagtca	ccgtcnatna	aacctgtggc	tggttctgtc	ttccgctcgc	180
tgtgaaagga	tctccagaag	gagtgtctga	tcttccccac	acttttgatg	actttattga	240
gtcgattctg	catgtccagc	aggaggttgt	accagctctc	tgacagtgag	gtcaccagcc	300
ctatcatgcc	nttgaacgtg	ccgaagaaca	ccgagccttg	tgtggggggg	gnagtctcac	360
ccagattctg	cattaccaga	nagccgtggc	aaaaganatt	gacaactcgc	ccaggnggaa	420
aaagaacacc	tcctggaagt	gctngccgct	cctcgtccnt	tggtggnnng	gcntnccttt	480
t						481

<210> 86

<211> 472

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(472)

<223> n = A,T,C or G

<400> 86

aacatcttcc	tgtataatgc	tgtgtaatat	cgatccgatn	ttgtctgctg	agaattcatt	60
acttggaaaa	gcaacttnaa	gcctggacac	tggtattaaa	attcacaata	tgcaacactt	120
taaacagtgt	gtcaatctgc	tcccttactt	tgatcatcacc	agtctgggaa	taagggtatg	180
ccctattcac	acctgttaaa	agggcgctaa	gcatttttga	ttcaacatct	ttttttttga	240
cacaagtccg	aaaaaagcaa	aagtaaacag	ttnttaattt	gtagccaat	tcactttctt	300
catgggacag	agccatttga	tttaaaaagc	aaattgcata	atattgagct	ttgggagctg	360
atatntgagc	ggaagantag	cctttctact	tcaccagaca	caactccttt	catattggga	420
tgtnnacnaa	agttatgtct	cttacagatg	ggatgctttt	gtggcaattc	tg	472

<210> 87

<211> 413

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(413)

<223> n = A,T,C or G

<400> 87

agaaaccagt	atctctnaaa	acaacctctc	ataccttggt	gacctaat	ttgtgtgcgtg	60
ttgtgtgtgc	cgcatattat	atagacaggc	acatcttttt	tacttttcta	aaagcttatg	120
cctcttttgt	atctatatct	gtgaaagt	taatgatctg	ccataatgtc	ttggggacct	180
ttgtcttctg	tgtaaatgg	actagagaaa	acacctatnt	tatgagtcaa	tctagttngt	240
tttattcgac	atgaaggaaa	tttccagatn	acaacactna	caaactctcc	cttgactagg	300
ggggacaaa	aaaagcnaaa	ctgaacatna	gaaacaattn	cctgggtgaga	aattncataa	360
acagaaattg	ggtngtatat	tgaaanann	catcattnaa	acgttttttt	ttt	413

<210> 88

<211> 448

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(448)

<223> n = A,T,C or G

<400> 88
 cgcagcgggt cctctctatc tagctccagc ctctcgctg ccccaactccc cgcgtcccgc 60
 gtcctagccn accatggccg ggcccctgcg cgcccgcgtg ctccctgctg ccatcctggc 120
 cgtggccctg gccgtgagcc cgcgcggccg ctccagctcc ggcaagccgc cgcgcctggt 180
 gggaggccca tggaccccg cgtggaagaag aagggtgtgcg gcgtgcactg gactttgccg 240
 tcggcnanta caacaaaccc gcaacnactt ttaccnagcn cgcgctgcag gttgtgccgc 300
 cccaancaaa ttgttactng gggtaantaa ttcttggaag ttgaacctgg gccaaacnng 360
 tttaccagaa ccnagccaat tngaacaatt ncccctccat aacagcccct tttaaaaagg 420
 gaancantcc tgntcttttc caaatattt 448

<210> 89
 <211> 463
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(463)
 <223> n = A,T,C or G

<400> 89
 gaattttgtg cactggccac tgtgatggaa ccattgggcc aggatgcttt gagtttatca 60
 gtagtgattc tgccaaagtt ggtgttgtaa catgagtatg taaaatgtca aaaaattagc 120
 agaggtctag gtctgcatat cagcagacag tttgtccgtg tattttgtag ccttgaagtt 180
 ctcaagtaca agttntttct gatgcgaagt tctnattcca gtgttttagt cctttgcac 240
 tttnatgttn agacttgccct ctntnaaatt gcttttgtnt tctgcaggta ctatctgtgg 300
 ttttaacaaaa tagaannact tctctgcttn gaanatttga atatcttaca tctnaaaatn 360
 aattctctcc ccatannaaa acccangccc ttggganaat ttgaaaaang gntccttcnn 420
 aattcnana anttcagntn tcatacaaca naacngganc ccc 463

<210> 90
 <211> 400
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(400)
 <223> n = A,T,C or G

<400> 90
 agggattgaa ggtctnttnt actgtcggac tgttcancca ccaactctac aagttgctgt 60
 cttccactca ctgtctgtaa gcntnttaac ccagactgta tcttcataaa tagaaciaat 120
 tcttcaccag tcacatcttc taggaccttt ttggattcag ttagtataag ctcttccact 180
 tcctttgtta agacttcac tggtaaagtc ttaagttttg tagaaaggaa ttttaattgct 240
 cgttctctaa caatgtcctc tcttgaagt atttgctga acaaccacc tnaagtcct 300
 ttgtgcatcc attttaaata tacttaatag ggcattggtg cactaggtta aattctgcaa 360
 gagtcatctg tctgcaaaaag ttgcgttagt atatctgcca 400

<210> 91
 <211> 480
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(480)
 <223> n = A,T,C or G

<400> 91
 gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60

ggctacccc	acatgggagc	agcatgccgt	agntatataa	ggtcattccc	tgagtcagac	120
atgcctcttt	gactaccgtg	tgccagtgtc	ggtgattctc	acacacctcc	nccgctctt	180
tgtggaaaaa	ctggcacttg	nctggaacta	gcaagacatc	acttacaaat	tcacccacga	240
gacacttgaa	aggtgtaaca	aagcgactct	tgcattgctt	tttgtccctc	cggcaccagt	300
tgtcaatact	aacccgctgg	tttgccctca	tcacatttgt	gatctgtagc	tctggatata	360
tctcctgaca	gtactgaaga	acttcttctt	ttgtttcaaa	agcaactctt	ggtgcctgtt	420
ngatcaggtt	cccatttccc	agtccgaatg	ttcacatggc	atatnttact	tcccacaaaa	480

<210> 92
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 92	
atacagccca	natcccacca
ggteccgctg	tagcccccagc
cccacgcagg	cagcagcggg
taantgcagg	aagaggctga
tgacgcgaaa	ctcctcgatg
gaaccttccg	cctgttctct
accagcggac	aaacggcggt
aggaacggcn	ccagcgtgtc
	caggtcaatg
	tcggtgaanc
	ctccgcgggt
	aatggcg
	60
	120
	180
	240
	300
	360
	420
	477

<210> 93
 <211> 377
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(377)
 <223> n = A,T,C or G

<400> 93	
gaacggctgg	accttgctc
agtccgagca	gccccagacc
cgcttcaatg	cagaaccant
tgattttact	tggaatttc
caacaacaaa	ataacatgtt
aagaaaatat	tactgttaca
ataaatatat	tattaaa
	60
	120
	180
	240
	300
	360
	377

<210> 94
 <211> 495
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(495)
 <223> n = A,T,C or G

<400> 94	
ccctttgagg	ggttagggc
cgagctgang	cagatttccc
ccaaggaaa	accacattct
gaaggcccca	ttccggggct
	cagttcccag
	tggaagaaac
	aggccaggag
	aantgcgtgc
	ggctatagtc
	tctgaccctt
	aggacctaga
	ggcaccaagg
	aggggctctg
	tgtgcccccc
	60
	120
	180
	240

acgaggaana	ggccctgant	cctgggatca	nacacccctt	cacgtgtatc	cccacacaaa	300
tgcaagctca	ccaaggtccc	ctctcagtc	cttcocctaca	ccctgaacgg	ncactggccc	360
acacccaccc	agancancca	cccgccatgg	ggaatgtnc	caaggaatcg	cngggcaacg	420
tggactctng	tcccnnaagg	gggcagaatc	tccaatagan	gganngaacc	cttgctnana	480
aaaaaaaaa	aaaaa					495

<210> 95
 <211> 472
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(472)
 <223> n = A,T,C or G

<400> 95						
ggttacttgg	tttcattgcc	accacttagt	ggatgtcatt	tagaaccatt	ttgtctgctc	60
cctctggaag	ccttgccgag	agcggacttt	gtaattgttg	gagaataact	gctgaatttt	120
tagctgtttt	gagttgattc	gcaccactgc	accacaactc	aatatgaaaa	ctatttnact	180
tattttattat	cttgtgaaaa	gtatacaatg	aaaattttgt	tcatactgta	tttatcaagt	240
atgatgaaaa	gcaatagata	tatattcttt	tattatgttn	aattatgatt	gccattatta	300
atcggcaaaa	tgtggagtg	atgttctttt	cacagtaata	tatgcctttt	gtaacttcac	360
ttggttattt	tattgtaaat	gaattacaaa	attcttaatt	taagaaaatg	gtangttata	420
tttanttcan	taatttcttt	ccttgtttac	gttaattttg	aaaagaatgc	at	472

<210> 96
 <211> 476
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(476)
 <223> n = A,T,C or G

<400> 96						
ctgaagcatt	tcttcaaact	tntctacttt	tgctattgat	acctgtagta	agttgacaat	60
gtggtgaaat	ttcaaaaatta	tatgtaactt	ctactagttt	tactttctcc	cccaagtctt	120
ttttaactca	tgattttttac	acacacaatc	cagaacttat	tatatagcct	ctaagtcttt	180
attcttcaca	gtagatgatg	aaagagtcct	ccagtgtcct	gngcanaatg	ttctagntat	240
agctggatac	atacngtggg	agttctataa	actcatacct	cagtgggact	naacccaaaat	300
tgtgttagtc	tcaattccta	ccacactgag	ggagcctccc	aaatcactat	attcttatct	360
gcaggtactc	ctccagaaaa	acngacaggg	caggcttgca	tgaaaaagtn	acatctgcgt	420
tacaaagtct	atcttctctca	nangtctgtn	aaggaacaat	ttaatcttct	agcttt	476

<210> 97
 <211> 479
 <212> DNA
 <213> Homo sapien

 <220>
 <221> misc_feature
 <222> (1)...(479)
 <223> n = A,T,C or G

<400> 97						
actctttcta	atgctgatat	gatcttgagt	ataagaatgc	atatgtcact	agaatggata	60
aaataatgct	gcaaaactta	tgttcttatg	caaaatggaa	cgctaagtga	acacagctta	120
caatcgcaaa	tcaaaaactca	caagtgtctca	tctgtgttag	atttagtgta	ataagactta	180
gattgtgctc	cttcggatat	gattgtttct	canatcttgg	gcaatnttcc	ttagtcaaat	240
caggctacta	gaattctggt	attggatatn	tgagagcatg	aaatttttaa	naatacactt	300

gtgattatna	aattaatcac	aaattttcact	tatacctgct	atcagcagct	agaaaaacat	360
ntnnntttta	natcaaagta	ttttgtgttt	ggaantgtnn	aaatgaaatc	tgaatgtggg	420
ttcnatctta	ttttttcccn	gacnactant	tnctttttta	gggncatttc	tganccatc	479

```
<210> 98
<211> 461
<212> DNA
<213> Homo sapien
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<400> 98							
agtgacttgt	cctccaacaa	aaccacctga	tcaagtttgt	ggcactgaca	atcagaccta		60
tgctagtctc	tgctacttat	tcgctactaa	atgcagactg	gagggggacca	aaaaggggga		120
tcaactccag	ctggattatt	ttggagcttg	caaatctatt	cctactttgt	cggactttga		180
agtgattcag	tttctcttac	ggatgagaga	ctggctcaag	aatatcctca	tcgagcttta		240
tgaagccact	ctgaacacgc	tggttatcta	gatgagaaca	gagaaataaa	gtcagaaaat		300
ttacctggag	aaagagggct	ttggctgggg	accatcccat	tgaaaccttct	cttaaggact		360
ttaagaaaaa	ctaccacatg	ttgtgtatcc	tggtgcgggc	cgtttatgaa	ctgaccaccc		420
tttgaataaa	ctttgacgtg	cctgaacctg	ctcctctcgg	a			461

```
<210> 99
<211> 171
<212> DNA
<213> Homo sapien
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<400> 99						
gtggcgcgcg	gcaggtgttt	cctcgtagcg	cagggccccc	tcccttcccc	aggcgccctt	60
cgggcgctct	gcgggcccga	ggaggagcgg	ctggcggggtg	gggggagtg	gacccacctt	120
cggtgagaaa	agccttctct	agcgatctga	gaggcggtgcc	ttgggggtac	c	171

```
<210> 100
<211> 269
<212> DNA
<213> Homo sapien
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<400> 100						
cggccgcaag	tgcaactcca	gctggggccg	tgcggaacaa	gattctgcc	gcagttggct	60
cgactgcgac	gacggcgcg	gcgacagtcg	caggtgcagc	gcggggcgct	gggggtcttg	120
aaggctgagc	tgacgccga	gaagtcgtgt	cacgtccac	gacctgacg	ccgtcgggga	180
cagccggaac	agagcccggt	gaagcgggag	gcctcgggga	gccctcggg	aagggcggcc	240
cgagagatac	gcaggtgcag	gtggcggcc				269

```
<210> 101
<211> 405
<212> DNA
<213> Homo sapien
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<400> 101						
tttttttttt	ttttggaatc	tactgcgagc	acagcaggtc	agcaacaagt	ttatttttgc	60
gctagcaagg	taacagggtg	gggcatgggt	acatgttctg	gtcaactttc	tttgtcgtgg	120
ttgattgggt	tgcttttatg	ggggcggggt	gggttagggg	aaacgaagca	aataacattg	180
agtgggtgca	ccctccctgt	agaacctggg	tacaaagctt	ggggcagttc	acctgggtctg	240
tgaccgtcat	tttcttgaca	tcaattgttat	tagaagtcat	gatatctttt	agagagtcca	300
ctgtttctgga	gggagattag	gggtttcttg	cataatccaac	aaaatccact	gaaaaagttg	360
qatgatcagt	acqaataccg	agqcataatt	ctcatatcggt	ggcca		405

```
<210> 102
<211> 470
<212> DNA
<213> Homo sapien
```

```

<400> 102
+++++ 60

```

ggcacttaat	ccatttttat	ttcaaaatgt	ctacaaattt	aatcccatta	tacgggtattt	120
tcaaaatcta	aattattcaa	attagccaaa	tccttaccaa	ataataccca	aaaatcaaaa	180
atatacttct	ttcagcaaac	ttgttacata	aattaaaaaa	atatatacgg	ctgggtgtttt	240
caaagtacaa	ttatcttaac	actgcaaaaca	ttttaaggaa	ctaaaataaa	aaaaaacact	300
ccgcaaagggt	taaagggaac	aacaaattct	tttacaacac	cattataaaa	atcatatctc	360
aaatcttagg	ggaatatata	cttcacacgg	gatcttaact	tttactcact	ttgttttattt	420
ttttaacca	ttgtttgggc	ccaacacaat	ggaatcccc	ctggactagt		470

<210> 103
 <211> 581
 <212> DNA
 <213> Homo sapien

<400> 103						
tttttttttt	ttttttttga	ccccctctt	ataaaaaaca	agttaccatt	ttattttact	60
tacacatatt	tattttataa	ttggtattag	atattcaaaa	ggcagctttt	aaaatcaaac	120
taaattgaaa	ctgccttaga	tacataattc	ttaggaatta	gcttaaaatc	tgccataaagt	180
gaaaatcttc	tctagctctt	ttgactgtaa	atttttgact	cttgtaaaac	atccaaattc	240
atttttcttg	tctttaaaat	tatctaattc	ttccattttt	tccttattcc	aagtcaattt	300
gcttctctag	cctcatttcc	tagctcttat	ctactattag	taagtggctt	ttttcctaaa	360
agggaaaaaa	ggaagagaaa	tggcacacaa	aacaaacatt	ttatattcat	atctctacct	420
acgttaataa	aatagcattt	tgtgaagcca	gctcaaaaaga	aggcttagat	ccttttatgt	480
ccattttagt	cactaaacga	tatcaaagt	ccagaatgca	aaaggtttgt	gaacatttat	540
tcaaaagcta	atataagata	tttcacatac	tcattcttct	g		581

<210> 104
 <211> 578
 <212> DNA
 <213> Homo sapien

<400> 104						
tttttttttt	tttttttttt	tttttctctt	cttttttttt	gaaatgagga	tcgagttttt	60
cactctctag	atagggcatg	aagaaaactc	atctttccag	ctttaaaata	acaatcaaat	120
ctcttatgct	atatcatatt	ttaagttaaa	ctaagtgc	actggcttat	cttctcctga	180
aggaaatctg	ttcattcttc	tcattcatat	agttatatca	agtactacct	tgcatattga	240
gaggtttttc	ttctctattt	acacatatat	ttccatgtga	atttgtatca	aacctttatt	300
ttcatgcaaa	ctagaaaata	atgtttcttt	tgcataagag	aagagaacaa	tatagcatta	360
caaaactgct	caaattgttt	gttaagtatt	ccattataat	tagttggcag	gagctaatac	420
aaatcacatt	tacgacagca	ataataaaac	tgaagtacca	gttaaatatc	caaaataatt	480
aaaggaaacat	ttttagcctg	ggtataatta	gctaattcac	tttacaagca	tttattagaa	540
tgaattcaca	tgttattatt	cctagcccaa	cacaatgg			578

<210> 105
 <211> 538
 <212> DNA
 <213> Homo sapien

<400> 105						
tttttttttt	tttttcagta	ataatcagaa	caatattttat	ttttatattt	aaaattcata	60
gaaaagtgcc	ttacatttaa	taaaagtgtg	tttctcaaag	tgatcagagg	aattagatat	120
gtcttgaaca	ccaatatata	tttgaggaaa	atacaccaaa	atacattaag	taaattattt	180
aagatcatag	agcttgtaag	tgaaaagata	aaatttgacc	tcagaaactc	tgagcattaa	240
aaatccacta	ttagcaataa	aattactatg	gacttcttgc	tttaattttg	tgatgaatat	300
ggggtgtcac	tggtaaacca	acacattctg	aaggatacat	tacttagtga	tagattctta	360
tgtactttgc	taatacgtgg	atatgagttg	acaagtctct	ctttcttcaa	tcttttaagg	420
ggcgagaaat	gaggaagaaa	agaaaaggat	tacgcatact	gttctttcta	tggaaggatt	480
agatatgttt	cctttgcca	tattaaaaaa	ataataatgt	ttactactag	tgaaaccc	538

<210> 106
 <211> 473
 <212> DNA
 <213> Homo sapien

<400> 106
 tttttttttt ttttttagtc aagtttctat tttttattata attaaagtct tgggtcatttc 60
 attttattagc tctgcaactt acatatatttaa attaaagaaa cgttttagac aactgtacaa 120
 tttataaatg taaggtgcca ttattgagta atatatctct ccaagagtgg atgtgtccct 180
 tctccacca actaatgaac agcaacatta gttaattttt attagtagat atacactgct 240
 gcaaacgcta attctcttct ccattcccat gtgatattgt gtatatgtgt gagttggtag 300
 aatgcatcac aatctacaat caacagcaag atgaagctag gctgggcttt cggtgaaaat 360
 agactgtgtc tgtctgaatc aaatgatctg acctatcctc ggtggcaaga actcttcgaa 420
 ccgcttcctc aaaggcgctg ccacatttgt ggctctttgc acttgtttca aaa 473

<210> 107
 <211> 1621
 <212> DNA
 <213> Homo sapien

<400> 107
 cgccatggca ctgcagggca tctcggtcat ggagctgtcc ggccctggccc cggggccggtt 60
 ctgtgctatg gtcctggctg acttcggggc gcgtgtggtg cgcgtggacc ggcccggctc 120
 ccgctacgac gtgagccgct tgggcccggg caagcgctcg ctagtgtggt acctgaagca 180
 gccgcgggga gccgccgtgc tgcggcgctc gtgcaagcgg tcggatgtgc tgcgtggagcc 240
 cttccgccgc ggtgtcatgg agaaactcca gctgggcccga gagattctgc agcgggaaaa 300
 tccaaggctt atttatgcca ggctgagtggt atttgggccag tcaggaagct tctgccgggt 360
 agctggccac gatatacaat atttggtctt gtcagggtgt ctctcaaaaa ttggcagaag 420
 tgggtgagaat ccgtatgccc cgctgaatct cctggctgac tttgctggtg gtggccttat 480
 gtgtgcactg ggcattataa tggctctttt tgaccgcaca cgcactgaca agggtcaggt 540
 cattgatgca aatatggtgg aaggaacagc atattttaagt tcttttctgt ggaaaactca 600
 gaaatcgagt ctgtgggaag cacctcgagg acagaacatg ttggatggtg gagcaccttt 660
 ctatacgact taacggacag cagatgggga attcatggct gttggagcaa tagaaccaca 720
 gttctacgag ctgctgatca aaggacttgg actaaagtct gatgaactc ccaatcagat 780
 gagcatggat gattggccag aaatgaagaa gaagtttgca gatgtatttg caaagaagac 840
 gaaggcagag tgggtgtcaa tctttgacgg cacagatgcc tgtgtgactc cggttctgac 900
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 cagccgcgaa gagatttatc agcttaactc agataaaatc attgaaagta ataaggtaaa 1140
 agctagtctc taacttccag gccacggct caagtgaatt tgaatactgc atttacagt 1200
 tagagtaaca cataacattg tatgcatgga aacatggagg aacagtatta cagtgtccta 1260
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 aatggttatc attagggtct ttgatttata aaactttggg tacttatact aaattatggt 1380
 agttattctg ccttccagtt tgcttgatat atttggtgat attagattc ttgacttata 1440
 ttttgaatgg gttctagtga aaaaggaatg atatatctt gaagacatcg atatacatt 1500
 atttacactc ttgattctac aatgtagaaa atgaggaaat gccacaaatt gtatggtgat 1560
 aaaagtcacg tgaacaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
 a 1621

<210> 108
 <211> 382
 <212> PRT
 <213> Homo sapien

<400> 108
 Met Ala Leu Gln Gly Ile Ser Val Met Glu Leu Ser Gly Leu Ala Pro
 1 5 10 15
 Gly Pro Phe Cys Ala Met Val Leu Ala Asp Phe Gly Ala Arg Val Val
 20 25 30
 Arg Val Asp Arg Pro Gly Ser Arg Tyr Asp Val Ser Arg Leu Gly Arg
 35 40 45
 Gly Lys Arg Ser Leu Val Leu Asp Leu Lys Gln Pro Arg Gly Ala Ala
 50 55 60
 Val Leu Arg Arg Leu Cys Lys Arg Ser Asp Val Leu Leu Glu Pro Phe
 65 70 75 80

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<210> 109
<211> 1524
<212> DNA
<213> Homo sapien
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<400> 109						
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gggcctggcc	atgcctcact	gagccagcgc	ctgcgcctct	acctcgccga	cagctggaac	120
cagtgcgacc	tagtggctct	cacctgcttc	ctctctggcg	tgggctgcgc	gctgaccccg	180
ggtttgtacc	acgtggcgccg	cactgtcttc	tgcctcgact	tcattggttt	cacgggtcgg	240
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<210> 110

<211> 3410

<212> DNA

<213> Homo sapien

<400> 110

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<210> 111

<211> 1289

<212> DNA

<213> Homo sapien

<400> 111

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tgaagatctt	cgggcccactg	tcgtccagtg	ccatgcagtt	tgtcaacgtg	ggctacttcc	300
tcacgcagc	cggcggtgtg	gtctttgtct	ttggtttctc	gggctgctat	ggtgctaaga	360
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tgttacaatg	ttaaaaaaa	aaaaaaaaa				1289

<210> 112

<211> 315

<212> PRT

<213> Homo sapien

<400> 112

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Leu	Gly	Pro	Lys	Ile	Val	Ile	Val	Ser	Lys	Met	Met	Lys	Asp	Val	Phe
			20					25					30		
Phe	Phe	Leu	Phe	Phe	Leu	Gly	Val	Trp	Leu	Val	Ala	Tyr	Gly	Val	Ala
		35				40					45				
Thr	Glu	Gly	Leu	Leu	Arg	Pro	Arg	Asp	Ser	Asp	Phe	Pro	Ser	Ile	Leu
	50					55					60				
Arg	Arg	Val	Phe	Tyr	Arg	Pro	Tyr	Leu	Gln	Ile	Phe	Gly	Gln	Ile	Pro
	65				70					75				80	
Gln	Glu	Asp	Met	Asp	Val	Ala	Leu	Met	Glu	His	Ser	Asn	Cys	Ser	Ser
			85					90						95	
Glu	Pro	Gly	Phe	Trp	Ala	His	Pro	Pro	Gly	Ala	Gln	Ala	Gly	Thr	Cys
			100					105					110		
Val	Ser	Gln	Tyr	Ala	Asn	Trp	Leu	Val	Val	Leu	Leu	Leu	Val	Ile	Phe

115	120	125
Leu Leu Val Ala Asn Ile	Leu Leu Val Asn Leu	Leu Ile Ala Met Phe
130	135	140
Ser Tyr Thr Phe Gly Lys	Val Gln Gly Asn Ser	Asp Leu Tyr Trp Lys
145	150	155
Ala Gln Arg Tyr Arg Leu	Ile Arg Glu Phe His	Ser Arg Pro Ala Leu
165	170	175
Ala Pro Pro Phe Ile Val	Ile Ser His Leu Arg	Leu Leu Arg Gln
180	185	190
Leu Cys Arg Arg Pro Arg	Ser Pro Gln Pro Ser	Ser Pro Ala Leu Glu
195	200	205
His Phe Arg Val Tyr Leu	Ser Lys Glu Ala Glu	Arg Lys Leu Leu Thr
210	215	220
Trp Glu Ser Val His Lys	Glu Asn Phe Leu Leu	Ala Arg Ala Arg Asp
225	230	235
Lys Arg Glu Ser Asp Ser	Glu Arg Leu Lys Arg	Thr Ser Gln Lys Val
245	250	255
Asp Leu Ala Leu Lys Gln	Leu Gly His Ile Arg	Glu Tyr Glu Gln Arg
260	265	270
Leu Lys Val Leu Glu Arg	Glu Val Gln Gln Cys	Ser Arg Val Leu Gly
275	280	285
Trp Val Ala Glu Ala Leu	Ser Arg Ser Ala Leu	Leu Pro Pro Gly Gly
290	295	300
Pro Pro Pro Pro Asp Leu	Pro Gly Ser Lys Asp	315
305	310	

<210> 113
 <211> 553
 <212> PRT
 <213> Homo sapien

<400> 113
Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
1 5 10 15
Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
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Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
35 40 45
Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
50 55 60
Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
65 70 75 80
Arg Tyr Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
85 90 95
Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
100 105 110
Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly
115 120 125
Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
130 135 140
Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
145 150 155 160
Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
165 170 175
Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
180 185 190
Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
195 200 205
Thr Cys Val Ala Ala Thr Leu Val Ala Glu Glu Ala Ala Leu Gly
210 215 220
Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
225 230 235 240

40

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255
 Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270
 Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285
 Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300
 Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320
 Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335
 Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350
 Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Gly Ala
 355 360 365
 Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380
 Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400
 Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415
 Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430
 Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445
 Gly Gly Ser Gly Leu Leu Pro Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460
 Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480
 Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495
 Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510
 Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525
 Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp
 530 535 540
 Lys Ser Asp Leu Ala Lys Tyr Ser Ala
 545 550

<210> 114

<211> 241

<212> PRT

<213> Homo sapien

<400> 114

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 1 5 10 15
 Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val
 20 25 30
 Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser
 35 40 45
 Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly
 50 55 60
 Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr
 65 70 75 80
 Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Phe Ile Leu Leu Leu Ile
 85 90 95
 Phe Ile Ala Glu Val Ala Ala Ala Val Val Ala Leu Val Tyr Thr Thr
 100 105 110
 Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys

<400> 115						
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tgtggtttgtg	aatccactct	gctttttccc	catttggaa	agtcatctac	ccatctctga	180
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ttagtc						366

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<220>  
<221> misc_feature  
<222> (1)...(282)  
<223> n = A,T,C or G
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<400> 116									
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agacttttact	attttcatat	tttaagacac	atgatttatc	ctattttagt	aacctgggtc				180
atacgtttaa	caaaaggtaa	tgtaacacgc	agagaggatt	tgttggcaga	aaatctatgt				240
tcaatctnna	actattctna	tcacaagcat	ttctattcct	tt					282

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<210> 117
<211> 305
<212> DNA
<213> Homo sapien
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<220>  
<221> misc_feature  
<222> (1)...(305)  
<223> n = A,T,C or G
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<400> 117
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tatttatecct cctcctgaa acaattgcaa aataanacaa aatatatgaa acaattgcaa 120

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aataaggcaa aatatatgaa acaacaggtc tcgagatatt ggaaatcagt caatgaagga 180
tactgatccc tgatcactgt cctaatgcag gatgtgggaa acagatgagg tcacctctgt 240
gactgccccca gcttactgcc tgtagagagt ttctangctg cagttcagac agggagaaat 300
tggtt 305

```

```

<210> 118
<211> 71
<212> DNA
<213> Homo sapien

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<220>
<221> misc_feature
<222> (1)...(71)
<223> n = A,T,C or G

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```

<400> 118
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aantcctggg t 71

```

```

<210> 119
<211> 212
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(212)
<223> n = A,T,C or G

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```

<400> 119
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gaaaatgggg tgaaattggc caactttcta tnaacttatg ttggcaantt tgccaccaac 120
agtaagctgg cccttctaataaaaagaaaat tgaaagggtt ctactaanc ggaattaant 180
aatggantca aganactccc aggcctcagc gt 212

```

```

<210> 120
<211> 90
<212> DNA
<213> Homo sapien

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```

<220>
<221> misc_feature
<222> (1)...(90)
<223> n = A,T,C or G

```

```

<400> 120
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ctccgccggc gcagaacatg ctgggggtgt 90

```

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<210> 121
<211> 218
<212> DNA
<213> Homo sapien

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```

<220>
<221> misc_feature
<222> (1)...(218)
<223> n = A,T,C or G

```

```

<400> 121
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gaataagatt tgctaaaaga ttgggggcta aaacatggtt attgggagac atttctgaag 120

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 agcatanact tcatgtgggg atancagcta cccttgta 218

<210> 122
 <211> 171
 <212> DNA
 <213> Homo sapien

<400> 122
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 catttgtag ctcatggaac aggaagtcgg atgggtgggc atcttcagtg ctgcatgagt 120
 caccaccccg gcggggtcat ctgtgccaca ggtccctgtt gacagtgcg t 171

<210> 123
 <211> 76
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc feature
 <222> (1)...(76)
 <223> n = A,T,C or G

<400> 123
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 ttatcaanta ttgtgt 76

<210> 124
 <211> 131
 <212> DNA
 <213> Homo sapien

<400> 124
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 caatgtgctg ggtcatatgg aggggaggag actctaaaat agccaatttt attctcttgg 120
 ttaagatttg t 131

<210> 125
 <211> 432
 <212> DNA
 <213> Homo sapien

<400> 125
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 ctacagtctg catttggcag aaatgaagat gaatttggat taaatgagga tgctgaagat 180
 ttgcctcacc aaacaaaagt gaaacaactg agagaaaatt ttcaggaaaa aagacagtgg 240
 ctcttgaagt atcagtcact tttgagaatg tttcttagtt actgcatact tcatggatcc 300
 catggtgggg gtcttgcatc tgtaagaatg gaattgattt tgcttttgca agaattctcag 360
 caggaaacat cagaaccact attttctagc cctctgtcag agcaaaccctc agtgcctctc 420
 ctctttgctt gt 432

<210> 126
 <211> 112
 <212> DNA
 <213> Homo sapien

<400> 126
 acacaacttg aatagtaaaa tagaaactga gctgaaattt ctaattcact ttctaaccat 60
 agtaagaatg atatttcccc ccagggatca ccaaatattt ataaaaattt gt 112

<210> 127

<211> 54
<212> DNA
<213> Homo sapien
.
<400> 127
accacgaaac cacaacaag atggaagcat caatccactt gccaaagcaca gcag 54

<210> 128
<211> 323
<212> DNA
<213> Homo sapien

<400> 128
acctcattag taattgtttt gttgtttcat ttttttctaa tgtctcccct ctaccagctc 60
acctgagata acagaatgaa aatggaagga cagccagatt tctcctttgc tctctgctca 120
ttctctctga agtctagggt acccattttg gggacccatt ataggcaata aacacagttc 180
ccaaagcatt tggacagttt cttgttgtgt tttagaatgg ttttcctttt tcttagcctt 240
ttcctgcaaa aggctcactc agtcccttgc ttgctcagtg gactgggctc cccagggcct 300
aggctgcctt cttttccatg tcc 323

<210> 129
<211> 192
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(192)
<223> n = A,T,C or G

<400> 129
acatacatgt gtgtatatatt ttaaatatca cttttgtatc actctgactt tttagcatac 60
tgaaaacaca ctaacataat ttntgtgaac catgatcaga tacaacccaa atcattcatc 120
tagcacattc atctgtgata naaagatagg tgagtttcat ttccttcacg ttggccaatg 180
gataaacaaa gt 192

<210> 130
<211> 362
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(362)
<223> n = A,T,C or G

<400> 130
ccctttttta tggaatgagt agactgtatg tttgaanatt tanccacaac ctctttgaca 60
tataatgacg caacaaaaag gtgctgttta gtcctatggt tcagtttatg ccctgacaa 120
gtttccattg tgttttgccg atcttctggc taatcgtggt atcctccatg ttattagtaa 180
ttctgtattc ctttttgtaa acgcctggta gatgtaacct gctangaggc taactttata 240
cttatttaaa agctcttatt ttgtggtcac taaaatggca atttatgtgc agcactttat 300
tgcagcagga agcacgtgtg gggttggtgt aaagctcttt gctaattcta aaaagtaatg 360
gg 362

<210> 131
<211> 332
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 131

ctttttgaaa gatcgtgtcc actcctgtgg acatcttgtt ttaatggagt ttcccatgca	60
gtangactgg tatggttgca gctgtccaga taaaaacatt tgaagagctc caaatgaga	120
gttctcccag gttcgccctg ctgctccaag tctcagcagc agcctctttt aggaggcatc	180
ttctgaacta gattaaggca gcttgtaa atctgatgtgat ttgggtttatt atccaactaa	240
cttccatctg ttatcactgg agaaagccca gactcccan gacnggtacg gattgtgggc	300
atanaaggat tgggtgaagc tggcgttgtg gt	332

<210> 132

<211> 322

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(322)

<223> n = A,T,C or G

<400> 132

acttttgcca tttgtatat ataaacaatc ttgggacatt ctctgaaaa ctaggtgtcc	60
agtggctaag agaactcgat ttcaagcaat tctgaaagga aaaccagcat gacacagaat	120
ctcaaattcc caaacagggg ctctgtggga aaaatgaggg aggaccttg tatctcgggt	180
tttagcaagt taaaatgaan atgacaggaa aggccttatt atcaacaaag agaagagttg	240
ggatgcttct aaaaaaaact ttggtagaga aaataggaat gctnaatcct agggaagcct	300
gtaacaatct acaattgggtc ca	322

<210> 133

<211> 278

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(278)

<223> n = A,T,C or G

<400> 133

acaagccttc acaagtttaa ctaaattggg attaatcttt ctgtanttat ctgcataatt	60
cttggttttc tttccatctg gctcctgggt tgacaatttg tggaaacaac tctattgcta	120
ctatttaaaa aaaatcacaa atctttccct ttaagctatg ttnaattcaa actattcctg	180
ctattcctgt tttgtcaaag aaatttatatt tttcaaaaata tgtntatttg tttgatgggt	240
cccacgaaac actaataaaa accacagaga ccagcctg	278

<210> 134

<211> 121

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(121)

<223> n = A,T,C or G

<400> 134

gtttanaaaa cttgttttagc tccatagagg aaagaatggt aaactttgta ttttaaaaca	60
tgattctctg aggttaaact tgggtttcaa atgttatatt tacttgtatt ttgcttttgg	120
t	121

<210> 135

<211> 350
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(350)
 <223> n = A,T,C or G

<400> 135
 acttanaaacc atgcctagca catcagaatc cctcaaagaa catcagtata atcctataacc 60
 atancaagtg gtgactgggt aagcgtgcga caaaggctcag ctggcacatt acttgtgtgc 120
 aaacttgata cttttgttct aagtaggaac tagtatacag tncctaggan tggtagtcca 180
 ggggtgcccc caactcctgc agccgctcct ctgtgccagn ccctgnaagg aactttcgtc 240
 ccacctcaat caagccctgg gccatgctac ctgcaattgg ctgaacaaac gtttgctgag 300
 ttcccaagga tgcaaagcct ggtgctcaac tcctggggcg tcaactcagt 350

<210> 136
 <211> 399
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(399)
 <223> n = A,T,C or G

<400> 136
 tgtaccgtga agacgacaga agttgcatgg cagggacagg gcagggccga ggccagggtt 60
 gctgtgattg tatccgaata ntcctcgtga gaaaagataa tgagatgacg tgagcagcct 120
 gcagacttgt gtctgccttc aanaagccag acaggaaggc cctgcctgcc ttggctctga 180
 cctggcgccc agccagccag ccacaggtgg gcttcttcct tttgtgtgta caacnccaag 240
 aaaactgcag agggccaggg tcaggtgtna gtgggtangt gaccataaaa caccagggtc 300
 tcccaggaac ccgggcaaag gccatcccca cctacagcca gcatgcccac tggcgtgatg 360
 ggtgcagang gatgaagcag ccagntgttc tgctgtggt 399

<210> 137
 <211> 165
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(165)
 <223> n = A,T,C or G

<400> 137
 actggtgtgg tngggggtga tgctggtggt anaagttgan gtgacttcan gatggtgtgt 60
 ggaggaagtg tgtgaacgta gggatgtaga ngttttggcc gtgctaaatg agcttcggga 120
 ttggtgtgtc ccactggtgg tcactgtcat tgggtggggt cctgt 165

<210> 138
 <211> 338
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(338)
 <223> n = A,T,C or G

<400> 138

```

actcactgga atgccacatt cacaacagaa tcagaggtct gtgaaaacat taatggctcc      60
ttaactttctc cagtaagaat cagggacttg aaatggaaac gttaacagcc acatgcccaa      120
tgctgggcag tctcccatgc cttccacagt gaaagggctt gagaaaaatc acatccaatg      180
tcatgtgttt ccagccacac caaaagggtc ttgggggtgga gggctggggg catananggt      240
cangcctcag gaagcctcaa gttccattca gctttgccac tgtacattcc ccatntttaa      300
aaaaactgat gccttttttt tttttttttg taaaattc                               338

```

```

<210> 139
<211> 382
<212> DNA
<213> Homo sapien

```

```

<400> 139
gggaatcttg gtttttgga tctggtttgc ctatagccga ggccactttg acagaacaaa      60
gaaagggact tcgagtaaga aggtgattta cagccagcct agtgcccga gtaaggaga      120
attcaaacag acctcgtcat tctggtgtg agcctggctg gctcaccgcc tatcatctgc      180
atttgcctta ctcaggtgct accggactct ggcccctgat gtctgtagtt tcacaggatg      240
ccttatttgt cttctacacc ccacagggcc ccctacttct tcggatgtgt ttttaataat      300
gtcagctatg tgcccacatc tcttcatgc cctccctccc tttcctacca ctgctgagtg      360
gcctggaact tgtttaaagt gt                               382

```

```

<210> 140
<211> 200
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(200)
<223> n = A,T,C or G

```

```

<400> 140
accaaanctt ctttctgttg tgttngattt tactataggg gtttngcttn ttctaaanatt      60
acttttcatt taacancttt tgttaagtgt caggctgcac tttgctccat anaattattg      120
ttttcacatt tcaacttgta tgtgtttgtc tcttanagca ttggtgaaat cacatatttt      180
atattcagca taaaggagaa                               200

```

```

<210> 141
<211> 335
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(335)
<223> n = A,T,C or G

```

```

<400> 141
actttatttt caaaacactc atatgttgca aaaaacacat agaaaaataa agtttggttg      60
gggtgctgac taaacttcaa gtcacagact tttatgtgac agattggagc agggtttgtt      120
atgcatgtag agaaccctaa ctaatttatt aaacaggata gaaacaggct gtctgggtga      180
aatggttctg agaaccatcc aattcacctg tcagatgctg atanactagc tcttcagatg      240
tttttctacc agttcagaga tnggttaatg actanttcca atggggaaaa agcaagatgg      300
attcacaac caagtaattt taaacaaaga cactt                               335

```

```

<210> 142
<211> 459
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature

```

<222> (1)...(459)

<223> n = A,T,C or G

<400> 142

accagggttaa	tattgccaca	tatatacctt	ccaattgcgg	gctaaacaga	cgtgtattta	60
gggttggtta	aagacaaccc	agcttaatat	caagagaaat	tgtgacctt	catggagtat	120
ctgatggaga	aaacactgag	ttttgacaaa	tcttatttta	ttcagatagc	agtctgatca	180
cacatgggcc	aacaacactc	aaataataaa	tcaaataatna	tcagatgtta	aagattggtc	240
ttcaaacatc	atagccaatg	atgccccgct	tgcctataat	ctctccgaca	taaaaccaca	300
tcaacacctc	agtggccacc	aaaccattca	gcacagcttc	cttaactgtg	agctgtttga	360
agctaccagt	ctgagcacta	ttgactatnt	ttttcangct	ctgaatagct	ctagggatct	420
cagcangggg	gggaggaacc	agctcaacct	tggcgtant			459

<210> 143

<211> 140

<212> DNA

<213> Homo sapien

<400> 143

acatttcctt	ccaccaagtc	aggactcctg	gcttctgtgg	gagttcttat	cacctgaggg	60
aaatccaaac	agtctctcct	agaaaggaat	agtgtcacca	acccaccca	tctccctgag	120
accatccgac	ttccctgtgt					140

<210> 144

<211> 164

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(164)

<223> n = A,T,C or G

<400> 144

acttcagtaa	caacatacaa	taacaacatt	aagtgtatat	tgccatcttt	gtcattttct	60
atctatacca	ctctcccttc	tgaaaacaan	aatcactanc	caatcactta	tacaaatttg	120
aggcaattaa	tccatatttg	ttttcaataa	ggaaaaaaag	atgt		164

<210> 145

<211> 303

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(303)

<223> n = A,T,C or G

<400> 145

acgtagacca	tccaactttg	tatttgtaat	ggcaaacatc	cagnagcaat	tcctaaacaa	60
actggagggt	atttataccc	aattatccca	ttcattaaca	tgccctcctc	ctcaggctat	120
gcaggacagc	tatcataagt	cggcccaggc	atccagatac	taccatttgt	ataaacttca	180
gtaggggagt	ccatccaagt	gacaggtcta	atcaaaggag	gaaatggaac	ataagcccag	240
tagtaaaatn	ttgcttagct	gaaacagcca	caaaagactt	accgccgtgg	tgattaccat	300
caa						303

<210> 146

<211> 327

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(327)
 <223> n = A,T,C or G

<400> 146
 actgcagctc aattagaagt ggtctctgac ttctcatcanc ttctccctgg gctccatgac 60
 actggcctgg agtgactcat tgctctgggt gggtgagaga gctcctttgc caacaggcct 120
 ccaagtcagg gctgggattt gtttcctttc cacattctag caacaatatg ctggccactt 180
 cctgaacagg gagggtgga ggagccagca tggaacaagc tgccactttc taaagtagcc 240
 agacttgccc ctgggcctgt cacacctact gatgacctc tgtgcctgca ggatggaatg 300
 taggggtgag ctgtgtgact ctatggt 327

<210> 147
 <211> 173
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(173)
 <223> n = A,T,C or G

<400> 147
 acattgtttt ttgagataa agcattgana gagctctcct taacgtgaca caatggaagg 60
 actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt 120
 atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gtt 173

<210> 148
 <211> 477
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(477)
 <223> n = A,T,C or G

<400> 148
 acaaccactt tatctcatcg aatttttaac ccaaactcac tcaactgtgcc tttctatcct 60
 atgggatata ttatttgatg ctccatttca tcacacatat atgaataata cactcatact 120
 gccctactac ctgctgcaat aatcacattc ccttcctgtc ctgaccctga agccattggg 180
 gtggctcctag tggccatcag tccangcctg caccttgagc ccttgagctc cattgtcac 240
 nccanccac ctcaccgacc ccattcctct acacagctac ctcccttgctc tctaacccca 300
 tagattatnt ccaaattcag tcaattaagt tactattaac actctaccg acatgtccag 360
 caccactggt aagccttctc cagccaacac acacacacac acacncacac acacacatat 420
 ccaggcacag gctacctcat cttcacaatc accccttta ttaccatgct atgggtgg 477

<210> 149
 <211> 207
 <212> DNA
 <213> Homo sapien

<400> 149
 acagttgtat tataatatca agaaataaac ttgcaatgag agcattttaag agggaagaac 60
 taacgtatnt tagagagcca aggaaggttt ctgtggggag tgggatgtaa ggtggggcct 120
 gatgataaat aagagtcagc caggtaagtg ggtggtgtgg tatgggcaca gtgaagaaca 180
 tttcaggcag agggaacagc agtgaaa 207

<210> 150
 <211> 111
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(111)
 <223> n = A,T,C or G

<400> 150
 accttgatgtt cattgctgct ctgatggaaa cccaactatc taatttagct aaaacatggg 60
 cacttaaatg tggtcagtgt ttggacttgt taactantgg catctttggg t 111

<210> 151
 <211> 196
 <212> DNA
 <213> Homo sapien

<400> 151
 agcgcggcag gtcattatga acattccaga tacctatcat tactcgatgc tgttgataac 60
 agcaagatgg ctttgaactc agggtcacca ccagctattg gaccttacta tgaaaacccat 120
 ggataccaac cggaaaaccc ctatcccga cagcccactg tggccccac tgtctacgag 180
 gtgcatccgg ctcagt 196

<210> 152
 <211> 132
 <212> DNA
 <213> Homo sapien

<400> 152
 acagcacttt cacatgtaag aagggagaaa ttcctaaatg taggagaaa ataacagAAC 60
 cttccctttt tcattagtgt gtggaaacct gatgctttat gttgacagga atagaaccag 120
 gagggagttt gt 132

<210> 153
 <211> 285
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(285)
 <223> n = A,T,C or G

<400> 153
 acaanaccCa nganaggcca ctggccgtgg tgtcatggcc tccaaacatg aaagtgtcag 60
 cttctgctct tatgtcctca tctgacaact ctttaccatt tttatcctcg ctgagcagga 120
 gcacatcaat aaagtccaaa gtcttgact tggccttgcc ttggaggaag tcatcaacac 180
 cctggctagt gaggggtcgg cgccgtcctt ggatgacggc atctgtgaag tcgtgcacca 240
 gtctgcaggc cctgtggaag cgccgtccac acggagtnag gaatt. 285

<210> 154
 <211> 333
 <212> DNA
 <213> Homo sapien

<400> 154
 accacagtcc tgttggggcca gggcttcatg accctttctg tgaaaagcca tattatcacc 60
 accccaaatt tttccttaa tctctttaac tgaaggggtc agcctcttga ctgcaaagac 120
 cctaagccgg ttacacagct aactcccact ggccctgatt tgtgaaattg ctgctgacctg 180
 attggcacag gagtccaagg tgttcagctc cctcctccg tggaacgaga ctctgatttg 240
 agtttcacaa attctcgggc cacctcgtca ttgtcctct gaaataaaat ccggagaatg 300
 gtcaggcctg tctcatccat atggatcttc cgg 333

<210> 155

<211> 308
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(308)
 <223> n = A,T,C or G

<400> 155
 actggaata ataaaaccca catcacagtg ttgtgtcaaa gatcatcagg gcatggatgg 60
 gaaagtgtt tgggaactgt aaagtgccta acacatgatc gatgattttt gttataatat 120
 ttgaatcacg gtgcatacaa actctcctgc ctgctcctcc tgggccccag cccagcccc 180
 atcacagctc actgctctgt tcatccaggc ccagcatgta gtggctgatt cttcttggct 240
 gcttttagcc tccanaagtt tctctgaagc caaccaaacc tctangtga aggcatgctg 300
 gcctgtgt 308

<210> 156
 <211> 295
 <212> DNA
 <213> Homo sapien

<400> 156
 accttgctcg gtgcttggaa catattagga actcaaaata tgagatgata acagtgccta 60
 ttattgatta ctgagagaac tgtagacat ttagttgaag attttctaca caggaactga 120
 gaataggaga ttatgtttgg cctcatatt ctctcctatc ctcttgcct cattctatgt 180
 ctaatatatt ctcaatcaa taaggttagc ataatcagga aatcgaccaa ataccaatat 240
 aaaaccagat gtctatcctt aagattttca aatagaaaac aaattaacag actat 295

<210> 157
 <211> 126
 <212> DNA
 <213> Homo sapien

<400> 157
 acaagtttaa atagtgtgt cactgtgcat gtgctgaaat gtgaaatcca ccacatttct 60
 gaagagcaaa acaaattctg tcatgtaatc tctatcttgg gtcgtgggta tatctgtccc 120
 cttagt 126

<210> 158
 <211> 442
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(442)
 <223> n = A,T,C or G

<400> 158
 acccactggt cttggaaca cccatcctta atacgatgat ttttctgtcg tgtgaaaatg 60
 aanccagcag gctgccccta gtcagtcctt ccttccagag aaaaagagat ttgagaaagt 120
 gcctgggttaa ttcaccatta atttctctcc ccaaactctc tgagtcttcc cttaatattt 180
 ctggtggttc tgaccaaagc aggtcatggt ttgttgagca tttgggatcc cagtgaagta 240
 natgtttgta gccttgcata cttagccctt cccacgcaca aacggagtgg cagagtgggtg 300
 ccaaccctgt tttccagtc cacgtagaca gattcacagt gcggaattct ggaagctgga 360
 nacagacggg ctctttgcag agccgggact ctgagangga catgagggcc tctgcctctg 420
 tgttcattct ctgatgtcct gt 442

<210> 159
 <211> 498
 <212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 159

acttccaggt aacgttggtg tttccgttga gcctgaactg atgggtgacg ttgtaggttc	60
tccaacaaga actgaggttg cagagcggtg aggggaagagt gctgttccag ttgcacctgg	120
gctgctgtgg actgttggtg attcctcact acggcccaag gttgtggaac tggcanaaag	180
gtgtgttggt gganttgagc tggggcggtg gtggtagggt gtgggctctt caacaggggc	240
tgctgtggtg ccgggagtg aangtggtgt gtcacttgag cttggccagc tctggaaagt	300
antanattct tctgaaggc cagcgcttgt ggagctggca ngggtcantg ttgtgtgtaa	360
cgaaccagtg ctgctgtggg tgggtgtana tctccacaa agcctgaagt tatgggtgcn	420
tcaggtana atgtggttgc agtgtccctg ggcngctgtg gaaggttgta nattgtcacc	480
aagggaataa gctgtggt	498

<210> 160

<211> 380

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(380)

<223> n = A,T,C or G

<400> 160

acctgcatcc agcttccctg ccaaactcac aaggagacat caacctctag acagggaaac	60
agcttcagga tacttccagg agacagagcc accagcagca aaacaaatat tcccatgcct	120
ggagcatggc atagaggaag ctganaaatg tggggctctga ggaagccatt tgagtctggc	180
cactagacat ctcatcagcc acttgtgtga agagatgcc catgacccca gatgcctctc	240
ccacccttac ctccatctca cacacttgag ctttccactc tgtataattc taacatcctg	300
gagaaaaatg gcagtttgac cgaacctgtt cacaacggta gaggtgatt tctaacgaaa	360
cttgtagaat gaagcctgga	380

<210> 161

<211> 114

<212> DNA

<213> Homo sapien

<400> 161

actccacatc ccctctgagc aggcggttgt cgttcaaggt gtatttgcc ttgcctgtca	60
cactgtccac tggccctta tccacttggt gcttaatccc tcgaaagagc atgt	114

<210> 162

<211> 177

<212> DNA

<213> Homo sapien

<400> 162

actttctgaa tcgaatcaaa tgatacttag tgtagtttta atatcctcat atatatcaaa	60
gttttactac tctgataatt ttgtaaacca ggtaaccaga acatccagtc atacagcttt	120
tggatgata taacttgga ataacccagt ctggatgata ataaaactac tcaactgt	177

<210> 163

<211> 137

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature
 <222> (1)...(137)
 <223> n = A,T,C or G

<400> 163
 catttatata gacaggcgtg aagacattca cgacaaaaac gcgaaattct atcccgtgac 60
 canagaaggc agctacggct actcctacat cctggcgtgg gtggccttcg cctgcacctt 120
 catcagcggc atgatgt 137

<210> 164
 <211> 469
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(469)
 <223> n = A,T,C or G

<400> 164
 cttatcacaa tgaatgttct cctgggcagc gttgtgatct ttgccacctt cgtgacttta 60
 tgcaatgcat catgctatct catacctaat gagggagttc caggagattc aaccaggaaa 120
 tgcatggatc tcaaaggaaa caaacaccca ataaactcgg agtggcagac tgacaactgt 180
 gagacatgca cttgctacga aacagaaatt tcatgttgca cccttgtttc tacacctgtg 240
 ggttatgaca aagacaactg ccaaagaatc ttcaagaagg aggactgcaa gtatatcgtg 300
 gtggagaaga aggacccaaa aaagacctgt tctgtcagtg aatggataat ctaatgtgct 360
 tctagtaggc acagggtctc caggccaggc ctcattctcc tctggcctct aatagtcaat 420
 gattgtgtag ccatgcctat cagtaaaaag atntttgagc aaacacttt 469

<210> 165
 <211> 195
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(195)
 <223> n = A,T,C or G

<400> 165
 acagtttttt atanatatcg acattgccgg cacttggtgt cagtttcata aagctgggtg 60
 atccgctgtc atccactatt ccttggttag agtaaaaatt attcttatag cccatgtccc 120
 tgcaggccgc ccgccgtag ttctcgttcc agtcgtcttg gcacacaggg tgccaggact 180
 tcctctgaga tgagt 195

<210> 166
 <211> 383
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(383)
 <223> n = A,T,C or G

<400> 166
 acatcttagt agtggtggcac atcagggggc catcaggggc acagtcactc atagcctcgc 60
 cgaggctcga gtccacacca ccggtgtagg tgtgctcaat cttgggcttg gcgccacct 120
 ttggagaagg gatatgctgc acacacatgt ccacaaagcc tgtgaactcg ccaaagaatt 180
 ttgcagacc agcctgagca aggggcggat gttcagcttc agtcctctct tcgtcagggtg 240
 gatgccaaac tcgtctangg tccgtgggaa gctgggtgtc acntcaccta caacctgggc 300
 gangatctta taaagaggct ccnagataaa ctccacgaaa cttctctggg agctgctagt 360

nggggccttt ttggtgaact ttc

383

<210> 167
 <211> 247
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(247)
 <223> n = A,T,C or G

<400> 167
 acagagccag accttggcca taaatgaanc agagattaag actaaacccc aagtcganat 60
 tggagcagaa actggagcaa gaagtgggcc tggggctgaa gtagagacca aggccactgc 120
 tatanccata cacagagcca actctcaggc caaggcnatg gttggggcag anccagagac 180
 tcaatctgan tccaaagtgg tggctggaac actggtcatg acanaggcag tgactctgac 240
 tgangtc 247

<210> 168
 <211> 273
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(273)
 <223> n = A,T,C or G

<400> 168
 acttctaagt tttctagaag tggaaggatt gtantcatcc tgaaaatggg tttacttcaa 60
 aatccctcan ccttggtctt cactactgtc tatactgana gtgtcatgtt tccacaaagg 120
 gctgacacct gagcctgnat tttcactcat ccctgagaag ccctttccag taggggtggc 180
 aattcccaac ttccttgcca caagcttccc aggtttctc ccctggaaaa ctccagcttg 240
 agtcccgat acactcatgg gctgccctgg gca 273

<210> 169
 <211> 431
 <212> DNA
 <213> Homo sapien
 <220>
 <221> misc_feature
 <222> (1)...(431)
 <223> n = A,T,C or G

<400> 169
 acagccttgg cttccccaaa ctccacagtc tcagtgcaga aagatcatct tccagcagtc 60
 agctcagacc aggggtcaaag gatgtgacat caacagtctc tggtttcaga acaggttcta 120
 ctactgtcaa atgaccccc atacttcctc aaaggctgtg gtaagttttg cacaggtgag 180
 ggcagcagaa agggggtant tactgatgga caccatctc tctgtatact ccacactgac 240
 cttgccatgg gcaaaggccc ctaccacaaa aacaatagga tcaactgctg gcaccagctc 300
 acgcacatca ctgacaaccg ggatggaaaa agaantgcca actttcatac atccaactgg 360
 aaagtgatct gatactggat tcttaattac cttcaaaaag ttctgggggc catcagctgc 420
 tcgaacactg a 431

<210> 170
 <211> 266
 <212> DNA
 <213> Homo sapien
 <220>

<221> misc_feature
 <222> (1)...(266)
 <223> n = A,T,C or G

<400> 170
 acctgtgggc tgggctgtta tgccctgtgcc ggctgctgaa agggagttca gaggtggagc 60
 tcaaggagct ctgcaggcat tttgccaanc ctctccanag canagggagc aacctacact 120
 ccccgctaga aagacaccag attggagtcc tgggaggggg agttgggggtg ggcatttgat 180
 gtatacttgt cacctgaatg aangagccag agaggaanga gacgaanatg anattggcct 240
 tcaaagctag gggctctggca ggtgga 266

<210> 171
 <211> 1248
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1248)
 <223> n = A,T,C or G

<400> 171
 ggcagccaaa tcataaacgg cgaggactgc agcccgcact cgcagccctg gcaggcggca 60
 ctggtcatgg aaaacgaatt gttctgctcg ggcgtcctgg tgcattccgca gtgggtgctg 120
 tcagccgcac actgtttcca gaagtgaagt cagagctcct acaccatcgg gctgggcctg 180
 cacagtcttg aggccgacca agagccaggg agccagatgg tggaggccag cctctccgta 240
 cggcaccag agtacaacag acccttgctc gctaacgacc tcatgctcat caagttggac 300
 gaatccgtgt ccgagtctga caccatccgg agcatcagca ttgcttcgca gtgccctacc 360
 gcggggaact cttgcctcgt ttctggctgg ggtctgctgg cgaacggcag aatgcctacc 420
 gtgctgcagt gcgtgaacgt gtcggtgggt tctgaggagg tctgcagtaa gctctatgac 480
 ccgctgtacc accccagcat gttctgcgcc ggcggagggc aagaccagaa ggactcctgc 540
 aacggtgact ctggggggcc cctgatctgc aacgggtact tgcagggcct tgtgtcttcc 600
 ggaaaagccc cgtgtggcca agttggcgtg ccagggtgtct acaccaacct ctgcaaattc 660
 actgagtggg tagagaaaac cgtccaggcc agttaactct ggggactggg aacctatgaa 720
 attgaccccc aaatacatcc tgcggaagga attcaggaat atctgttccc agcccctcct 780
 ccctcaggcc caggagtcca ggccccagc ccctcctccc tcaaaccaag ggtacagatc 840
 cccagcccct cctccctcag acccaggagt ccagaccccc cagcccctcc tccctcagac 900
 ccaggagtcc agcccctcct ccctcagacc caggagtcca gacccccag cccctcctcc 960
 ctcagaccga ggggtccagg cccccaacc ctccctcctc agactcagag gtccaagccc 1020
 ccaaccntc attccccaaga cccagaggtc cagggtcccag cccctcntcc ctcagaccga 1080
 gcggtccaat gccacctaga ctntccctgt acacagtgcc cccttggtggc acgttgacct 1140
 aacctacca gttgtttttt catttttngt ccctttcccc tagatccaga aataaagttt 1200
 aagagaagng caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1248

<210> 172
 <211> 159
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(159)
 <223> Xaa = Any Amino Acid

<400> 172
 Met Val Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro
 1 5 10 15
 Leu Leu Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser
 20 25 30
 Glu Ser Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr
 35 40 45
 Ala Gly Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly

56

50	55	60
Arg Met Pro Thr Val	Leu Gln Cys Val Asn Val	Ser Val Val Ser Glu
65	70	75
Glu Val Cys Ser Lys	Leu Tyr Asp Pro Leu Tyr	His Pro Ser Met Phe
85	90	95
Cys Ala Gly Gly Gly	Gln Xaa Gln Xaa Asp Ser	Cys Asn Gly Asp Ser
100	105	110
Gly Gly Pro Leu Ile	Cys Asn Gly Tyr Leu Gln	Gly Leu Val Ser Phe
115	120	125
Gly Lys Ala Pro Cys	Gly Gln Val Gly Val Pro	Gly Val Tyr Thr Asn
130	135	140
Leu Cys Lys Phe Thr	Glu Trp Ile Glu Lys Thr	Val Gln Ala Ser
145	150	155

<210> 173
 <211> 1265
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1265)
 <223> n = A,T,C or G

<400> 173

ggcagccgc	actgcagcc	ctggcaggcg	gcactggtca	tggaaaacga	attgttctgc	60
tcgggcgctc	tggtgcatcc	gcagtgggtg	ctgtcagccg	cacactgttt	ccagaactcc	120
tacaccatcg	ggctgggcct	gcacagtctt	gaggccgacc	aagagccagg	gagccagatg	180
gtggaggcca	gcctctccgt	acggcaccca	gagtacaaca	gacccttgct	cgctaacgac	240
ctcatgctca	tcaagttgga	cgaatccgtg	tccgagtctg	acaccatccg	gagcatcagc	300
attgcttcgc	agtgccctac	cgcggggaac	tcttgccctg	tttctggctg	gggtctgctg	360
gcgaacggtg	agctcacggg	tgtgtgtctg	ccctcttcaa	ggaggtcctc	tgcccagtcg	420
cgggggctga	cccagagctc	tgcgctccag	gcagaatgcc	taccgtgctg	cagtgcgtga	480
acgtgtcggg	ggtgtctgag	gaggtctgca	gtaagctcta	tgaccgctg	taccaccca	540
gcattgtctg	cgccggcgga	gggcaagacc	agaaggactc	ctgcaacggg	gactctgggg	600
ggcccctgat	ctgcaacggg	tacttgacag	gccttgtgtc	tttcggaaaa	gccccgtgtg	660
gccaaagttg	cgtgccaggt	gtctacacca	acctctgcaa	attcactgag	tggaatagaga	720
aaaccgtcca	ggccagttaa	ctctggggac	tggaaccca	tgaaattgac	ccccaaatac	780
atcctgcgga	aggaattcag	gaatatctgt	tcccagcccc	tcctccctca	ggcccaggag	840
tccaggcccc	cagccctcc	tcctcaaac	caagggtaca	gatccccagc	ccctcctccc	900
tcagaccag	gagtcagac	ccccagccc	ctctccctc	agaccagga	gtccagcccc	960
tcctcctca	gaccaggag	tccagacccc	ccagccctc	ctccctcaga	cccagggtt	1020
gaggccccca	accctcctc	cttcagagtc	agaggtccaa	gcccccaacc	cctcgttccc	1080
cagaccaga	ggttnnagtc	ccagcccctc	ttcctcaga	cccagnngtc	caatgccacc	1140
tagattttcc	ctgnacacag	tgccccttg	tggnangttg	acccaacctt	accagttggt	1200
ttttcatttt	tngtcccttt	cccctagatc	cagaaataaa	gtttaagaga	ngngcaaaaa	1260
aaaaa						1265

<210> 174
 <211> 1459
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(1459)
 <223> n = A,T,C or G

<400> 174

ggtcagccgc	acactgtttc	cagaagtggg	tgacagctc	ctacaccatc	gggctggggc	60
tgacagctc	tgaggccgac	caagagccag	ggagccagat	ggtggaggcc	agcctctccg	120
tacggcacc	agagtacaac	agacccttgc	tcgtaacga	cctcatgctc	atcaagttgg	180

acgaatccgt	gtccgagtct	gacaccatcc	ggagcatcag	cattgcttcg	cagtgcctta	240
ccgcggggaa	ctcttgcttc	gtttctggct	ggggtctgct	ggcgaacggt	gagctcacgg	300
gtgtgtgtct	gccctcttca	aggaggtcct	ctgcccagtc	gcgggggctg	acccagagct	360
ctgcgtccca	ggcagaatgc	ctaccgtgct	gcagtgcgtg	aacgtgtcgg	tggtgtctga	420
ngaggtctgc	antaagctct	atgacccgct	gtaccacccc	ancatgttct	gcgccggcgg	480
agggcaagac	cagaaggact	cctgcaacgt	gagagagggg	aaaggggagg	gcaggcgact	540
caggggaagg	tggagaagg	ggagacagag	acacacaggg	ccgcatggcg	agatgcagag	600
atggagagac	acacagggag	acagtgcaca	ctagagagag	aaactgagag	aaacagagaa	660
ataaacacag	gaataaagag	aagcaaagga	agagagaaac	agaaacagac	atggggaggc	720
agaaacacac	acacatagaa	atgcagttga	ccttccaaca	gcatggggcc	tgagggcggt	780
gacctccacc	caatagaaaa	tectcttata	acttttgact	ccccaaaaac	ctgactagaa	840
atagcctact	gttgacgggg	agccttacca	ataacataaa	tagtgcattt	atgcatacgt	900
tttatgcatt	catgatatac	ctttgttgga	attttttgat	atttctaagc	tacacagttc	960
gtctgtgaat	ttttttaaat	tggtgcaact	ctcctaaaat	ttttctgatg	tgtttattga	1020
aaaaatccaa	gtataagtgg	acttgtgcat	tcaaaccagg	gttggtcaag	ggtcaactgt	1080
gtacccagag	ggaaacagtg	acacagattc	atagaggtga	aacacgaaga	gaaacaggaa	1140
aaatcaagac	tctacaaaga	ggctgggcag	ggtggctcat	gcctgtaatc	ccagcacttt	1200
gggaggcgag	gcaggcagat	cacttgaggt	aaggagttca	agaccagcct	ggccaaaatg	1260
gtgaaatcct	gtctgtacta	aaaatacaaa	agttagctgg	atatggtggc	aggcgccctgt	1320
aatcccagct	acttgggagg	ctgaggcagg	agaattgctt	gaatatggga	ggcagagggt	1380
gaagtgagtt	gagatcacac	cactatactc	cagctggggc	aacagagtaa	gactctgtct	1440
caaaaaaaaa	aaaaaaaaa					1459

<210> 175

<211> 1167

<212> DNA

<213> Homo sapien

<220>

<221> misc feature

<222> (1)...(1167)

<223> n = A,T,C or G

<400> 175

gcgcagccct	ggcaggcggc	actggtcagt	gaaaacgaat	tgttctgctc	gggcgtcctg	60
gtgcatccgc	agtgggtgct	gtcagccgca	cactgtttcc	agaactccta	caccatcggg	120
ctgggcctgc	acagtcttga	ggccgaccaa	gagccaggga	gccagatggt	ggaggccagc	180
ctctccgtac	ggcaccacaga	gtacaacaga	ctcttgctcg	ctaacgacct	catgctcatc	240
aagttggacg	aatccgtgtc	cgagtctgac	accatccgga	gcatcagcat	tgcttcgcag	300
tgccctacgc	cggggaaactc	ttgcctcgtn	tctggctggg	gtctgctggc	gaacggcaga	360
atgcctaccg	tgctgcactg	cgtgaacgtg	tcgggtggtg	ctgaggangt	ctgcagtaag	420
ctctatgacc	cgctgtacca	ccccagcatg	ttctgcgccg	gcggaggggca	agaccagaag	480
gactcctgca	acgggtgactc	tgggggggccc	ctgatctgca	acgggtactt	gcagggcctt	540
tggtctttcg	gaaaagcccc	gtgtggccaa	cttgccgtgc	caggtgtcta	caccaacctc	600
tgcaaattca	ctgagtggat	agagaaaacc	gtccagncca	gttaactctg	gggactggga	660
acccatgaaa	ttgacccccca	aatacatcct	gcggaangaa	ttcaggaata	tctgttccca	720
gccccctctc	cctcaggccc	aggagtccag	gccccagccc	cctcctccct	caaaccaagg	780
gtacagatcc	ccagcccttc	ctccctcaga	cccaggagtc	cagaccccc	agccccctnt	840
ccntcagacc	caggagtcca	gccccctctc	cntcagacgc	aggagtccag	accccccagc	900
ccntcntccg	tcagaccacg	gggtgcaggc	cccccaacccc	tentccntca	gagtcagagg	960
tccaagcccc	caaccctctg	ttccccagac	ccagaggtnc	aggtcccagc	ccctcctccc	1020
tcagaccacg	cggtccaatg	ccacctagan	tntccctgta	cacagtgcgc	ccttgtggca	1080
ngttgaccca	accttaccag	ttggtttttc	attttttgtc	cctttccccc	agatccagaa	1140
ataaagtnta	agagaagcgc	aaaaaaa				1167

<210> 176

<211> 205

<212> PRT

<213> Homo sapien

<220>

<221> VARIANT

<222> (1)...(205)

<223> Xaa = Any Amino Acid

<400> 176

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Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1      5      10      15
Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20      25      30
Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35      40      45
Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Leu Leu Leu
 50      55      60
Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65      70      75      80
Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85      90      95
Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100      105      110
Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115      120      125
Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130      135      140
Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145      150      155      160
Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165      170      175
Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180      185      190
Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195      200      205

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<210> 177

<211> 1119

<212> DNA

<213> Homo sapien

<400> 177

```

gcgcactcgc agccctggca ggcggcactg gtcatggaaa acgaattgtt ctgctcgggc      60
gtcctgggtgc atccgcagtg ggtgctgtca gccgcacact gtttccagaa ctccacacc      120
atcgggcttg gctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag      180
gccagcctct ccgtacggca cccagagtac aacagaccct tgctcgctaa cgacctcatg      240
ctcatcaagt tggacgaatc cgtgtccgag tctgacacca tccggagcat cagcattgct      300
tcgcagtgcc ctaccgcggg gaactcttgc ctcgtttctg gctgggtct gctggcgaa      360
gatgctgtga ttgccatcca gtcccagact gtgggaggct gggagtgtga gaagcttcc      420
caaccctggc agggttgtac catttcggca acttccagtg caaggacgtc ctgctgcatc      480
ctcactgggt gtcactact gtcactgca tcacccgaa cactgtgatc aactagccag      540
caccatagtt ctccgaagtc agactatcat gattactgtg ttgactgtgc tgtctattgt      600
actaaccatg ccgatgttta ggtgaaatta gcgtcacttg gcctcaacca tcttggtatc      660
cagttatcct cactgaattg agatttcctg cttcagtgtc agccattccc acataatttc      720
tgacctacag aggtgaggga tcatatagct cttcaaggat gctggtactc ccctcacaaa      780
ttcatttctc ctgtttagt gaaagggtcg ccctctggag cctcccaggg tgggtgtgca      840
ggtcacaaatg atgaatgtat gatcgtgttc ccattaccca aagcctttaa atccctcatg      900
ctcagtacac cagggcaggt ctagcatttc ttcatttagt gtatgctgtc cattcatgca      960
accacctcag gactcctgga ttctctgcct agttgagctc ctgcatgctg cctccttggg      1020
gaggtgaggg agagggccca tggttcaatg ggatctgtgc agttgtaaca cattaggtgc      1080
ttaataaaca gaagctgtga tgtaaaaaa aaaaaaaaaa      1119

```

<210> 178

<211> 164

<212> PRT

<213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(164)
 <223> Xaa = Any Amino Acid

<400> 178
 Met Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp
 1 5 10 15
 Val Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu
 20 25 30
 Gly Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val
 35 40 45
 Glu Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu
 50 55 60
 Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80
 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95
 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Asp Ala Val
 100 105 110
 Ile Ala Ile Gln Ser Xaa Thr Val Gly Gly Trp Glu Cys Glu Lys Leu
 115 120 125
 Ser Gln Pro Trp Gln Gly Cys Thr Ile Ser Ala Thr Ser Ser Ala Arg
 130 135 140
 Thr Ser Cys Cys Ile Leu Thr Gly Cys Ser Leu Leu Leu Thr Ala Ser
 145 150 155 160
 Pro Gly Thr Leu

<210> 179
 <211> 250
 <212> DNA
 <213> Homo sapien

<400> 179
 ctggagtgcc ttggtgtttc aagccctgc aggaagcaga atgcaccttc tgaggcacct 60
 ccagctgccc ccgcccggg gatgcgaggc tcggagcacc cttgccggc tgtgattgct 120
 gccaggcaact gttcatctca gcttttctgt ccctttgtc ccggcaagcg cttctgctga 180
 aagttcatat ctggagcctg atgtcttaac gaataaaggt cccatgctcc acccgaaaaa 240
 aaaaaaaaaa 250

<210> 180
 <211> 202
 <212> DNA
 <213> Homo sapien

<400> 180
 actagtccag tgtggtggaa ttccattgtg ttgggcccac cacaatggct acctttaaca 60
 tcaccagac ccgcccctg ccgctgccc acgctgctgc taacgacagt atgatgctta 120
 ctctgtact cggaaactat ttttatgtaa ttaatgtatg ctttcttgtt tataaatgcc 180
 tgatttaaaa aaaaaaaaaa aa 202

<210> 181
 <211> 558
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(558)
 <223> n = A,T,C or G

```

<400> 181
tccytttgkt naggttttkg agacamccck agacctwaan ctgtgtcaca gacttcyngg    60
aatgttttagg cagtgtctagt aatttcytcg taatgattct gttattactt tcctnattct    120
ttattcctct ttcttctgaa gattaatgaa gttgaaaatt gaggtggata aatacaaaaa    180
ggtagtgtga tagtataagt atctaagtgc agatgaaagt gtgttatata tatccattca    240
aaattatgca agttagtaat tactcagggt taactaaatt actttaatat gctgttgaac    300
ctactctgtt ccttggtctag aaaaaattat aaacaggact ttgttagttt gggaagccaa    360
attgataata ttctatgttc taaaagttgg gctatacata aattattaag aaatatggaw    420
ttttattccc aggaatatgg kgttcatttt atgaatatta cscrggatag awgtwtgagt    480
aaaaycagtt ttggtwaata ygtwaatatg tcmtaaataa acaakgcttt gacttatttc    540
caaaaaaaaa aaaaaaaa
558

```

```

<210> 182
<211> 479
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

```

```

<400> 182
acagggwttk grggatgcta agsccccrga rwtgytttga tccaaccctg gcttwttttc    60
agaggggaaa atggggccta gaagttacag mscatytagy tgggtgcgmtg gcacccttgg    120
cstcacacag astcccgagt agctgggact acaggcacac agtcaactgaa gcaggccctg    180
ttwgcaattc acgttgccac ctccaactta aacattcttc atatgtgatg tccttagtca    240
ctaagggttaa actttcccac ccagaaaagg caacttagat aaaatcttag agtactttca    300
tactmttcta agtcctcttc cagcctcact kkgagtcctm cytgggggtt gataggaant    360
ntctcttggc tttctcaata aartctctat ycatctcatg ttttaatttg tacgcatara    420
awtgstgara aaattaaaat gttctggtty mactttaaaa aaaaaaaaaa aaaaaaaaaa    479

```

```

<210> 183
<211> 384
<212> DNA
<213> Homo sapien

```

```

<400> 183
aggcgggagc agaagctaaa gccaaagccc aagaagagtg gcagtgccag cactgggtgcc    60
agtaccagta ccaataacag tgccagtgcc agtgccagca ccagtgggtg cttcagtgtc    120
ggtgccagcc tgaccgccac tctcacattt gggctcttcg ctggccttgg tggagctggt    180
gccagcacca gtggcagctc tgggtcctgt ggtttctcct acaagtgaga ttttagatat    240
tgttaatcct gccagtcttt ctcttcaagc cagggtgcat cctcagaaac ctactcaaca    300
cagcactcta ggcagccact atcaatcaat tgaagttgac actctgcatt aratctattt    360
gccatttcaa aaaaaaaaaa aaaa
384

```

```

<210> 184
<211> 496
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(496)
<223> n = A,T,C or G

```

```

<400> 184
accgaattgg gaccgtggc ttataagcga tcatgtyynt ccrgtatcac ctcaacgagc    60
aggagatcgc agtctatagc ctgaagaaat ttgaccgatg gggacaacag acctgctcag    120
cccatacctg tcggttctcc ccagatgaca aatactctsg acaccgaatc accatcaaga    180
aacgcttcaa ggtgctcatg acccagcaac cgcgcctgtg cctctgaggg tcccttaaac    240
tgatgtcttt tctgccacct gttaccctc ggagactccg taaccaaact cttcggaactg    300

```

```

tgagccctga tgcctttttg ccagccatac tctttggcat ccagtctctc gtggcgattg      360
attatgcttg tgtgaggcaa tcatggtggc atcaccataa aagggaacac atttgacttt      420
tttttctcat attttaaatt actacmagaw tattwmagaw waaatgawtt gaaaaactst      480
taaaaaaaaa aaaaaa                                     496

```

```

<210> 185
<211> 384
<212> DNA
<213> Homo sapien

```

```

<400> 185
gctggtagcc tatggcgkkg cccacggagg ggctcctgag gccacggrac agtgacttcc      60
caagtatcyt gcgscgctc ttctaccgtc cctacctgca gatcttcggg cagattcccc      120
aggaggacat ggacgtggcc ctcatggagc acagcaactg ytcgtcggag cccggcttct      180
gggcacaccc tcctggggcc caggcgggca cctgcgtctc ccagtatgcc aactggctgg      240
tggtgctgct cctcgtcatc ttctgctcg tggccaacat cctgctggtc aacttgctca      300
ttgccatgtt cagttacaca ttcggaagag tacagggcaa cagcgatctc tactgggaag      360
gcgcagcgtt accgcctcat ccgg                                     384

```

```

<210> 186
<211> 577
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(577)
<223> n = A,T,C or G

```

```

<400> 186
gagttagctc ctccacaacc ttgatgaggt cgtctgcagt ggcctctcgc ttcataccgc      60
tnccatcgtc atactgtagg tttgccacca cytcctggca tcttggggcg gcntaatatt      120
ccaggaaaact ctcaatcaag tcaccgtcga tgaaacctgt gggctgggtc tgtcttccgc      180
tcggtgtgaa aggatctccc agaaggagtg ctcgatcttc cccacacttt tgatgacttt      240
attgagtcca ttctgcatgt ccagcaggag gttgtaccag ctctctgaca gtgaggtcac      300
cagccctatc atgccgttga mcgtgccgaa garcaccgag ccttgtgtgg gggkkgaagt      360
ctcaccaga ttctgatta ccagagagcc gtggcaaaag acattgacaa actcgcccag      420
gtggaaaaag amcamctcct ggargtgctn gccgctctc gtcmgttggt ggcagcgctw      480
tccttttgac acacaaacaa gttaaaggca ttttcagccc ccagaaantt gtcacatcc      540
aagatntcgc acagactna tccagttggg attaaat                                     577

```

```

<210> 187
<211> 534
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(534)
<223> n = A,T,C or G

```

```

<400> 187
aacatcttcc tgtataatgc tgtgtaatat cgatccgatn ttgtctgstg agaatycatw      60
actkggaaaa gmaacattaa agcctggaca ctggtattaa aattcacaat atgcaacact      120
ttaaacagtg tgtcaatctg ctcccyynac tttgtcatca ccagtctggg aakaagggtg      180
tgccctattc acacctgtta aaagggcgct aagcattttt gattcaacat cttttttttt      240
gacacaagtc cgaaaaaagc aaaagtaaag agttatyaat ttgtagcga attcacttct      300
ttcatgggac agagccatyt gatttaaaaa gcaaatgca taatattgag ctttygggagc      360
tgatatttga gcggaagagt agcctttcta cttcaccaga cacaactccc tttcatattg      420
ggatgttnac naaagtwatg tctctwacag atgggatgct tttgtggcaa ttctgttctg      480
aggatctccc agtttattta ccacttgcaac aagaaggcgt tttcttctc aggc                                     534

```


62

<210> 188
 <211> 761
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(761)
 <223> n = A,T,C or G

<400> 188
 agaaaccagt atctctnaaa acaacctctc ataccttggtg gacctaatTT tgtgtgctg 60
 tgtgtgtgCG cgcataattat atagacaggc acatcttttt tacttttTta aaagcttatg 120
 cctctttTgt atctatatct gtgaaagtTT taatgatctg ccataatgtc ttggggacct 180
 ttgtcttctg tgtaaatggt actagagaaa acacctatnt tatgagtcaa tctagttngt 240
 tttattcgac atgaaggaaa tttccagatn acaactctna caaactctcc ctkgackarg 300
 ggggacaaag aaaagcaaaa ctgamcataa raaacaatwa cctggtgaga arttgcataa 360
 acagaaatwr ggtagtatat tgaarnacag catcattaaa rmgttwktt wttctccctt 420
 gcaaaaaaca tgtacngact tcccgttgag taatgccaaag ttgttttttt tatnataaaa 480
 cttgcccttc attacatggt tnaaagtggg gtggtggggc aaaatattga aatgatggaa 540
 ctgactgata aagctgtaca aataagcagt gtgcctaaca agcaacacag taatgttgac 600
 atgcttaatt cacaaatgct aatttcatta taaatgtttg ctaaaataca ctttgaacta 660
 tttttctgtn ttcccagagc tgagatntta gattttatgt agtatnaagt gaaaaantac 720
 gaaaataata acattgaaga aaaaanaaaa aaanaaaaaa a 761

<210> 189
 <211> 482
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(482)
 <223> n = A,T,C or G

<400> 189
 tttttttttt tttgccgatn ctactatttt attgcaggan gtgggggtgt atgcaccgca 60
 caccggggct atnagaagca agaaggaagg agggagggca cagccccttg ctgagcaaca 120
 aagcgcctg ctgccttctc tgtctgtctc ctggtgcagg cacatgggga gaccttcccc 180
 aaggcagggg ccaccagtcc aggggtggga atacagggg tgggagtgt gcataagaag 240
 tgataggcac aggccaccgg gtacagaccc ctcggtcctt gacaggtnga tttcgaccag 300
 gtcattgtgc cctgcccagg cacagcgtan atctggaaaa gacagaatgc tttccttttc 360
 aaatttggt ngtcatngaa ngggcanttt tccaanttng gctnggtctt ggtacnctt 420
 gttcggccca gtcncngtc caaaaantat tcaccnnct ccnaattgct tgcnggnccc 480
 cc 482

<210> 190
 <211> 471
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(471)
 <223> n = A,T,C or G

<400> 190
 tttttttttt ttttaaaaca gtttttcaca acaaaattta ttagaagaat agtggttttg 60
 aaaactctcg catccagtga gaactaccat acaccacatt acagctngga atgtnctcca 120
 aatgtctggt caaatgatac aatggaacca ttcaatctta cacatgcacg aaagaacaag 180
 cgcttttgac atacaatgca caaaaaaaa aggggggggg gaccacatgg attaaaattt 240
 taagtactca tcacatacat taagacacag ttctagtcca gtcnaaaatc agaactgcnt 300

```

tgaaaaattt catgtatgca atccaaccaa agaacttnat tggatgatcat gantncteta 360
ctacatcnac cttgatcatt gccaggaacn aaaagttnaa ancacnngt acaaaaaanaa 420
tctgtaattn anttcaacct ccgtacngaa aaatnttntt tatacactcc c 471

```

```

<210> 191
<211> 402
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(402)
<223> n = A,T,C or G

```

```

<400> 191
gagggattga aggtctgttc tastgtcggm ctgttcagcc accaactcta acaagttgct 60
gtcttccact cactgtctgt aagcttttta acccagacwg tatcttcata aatagaacaa 120
attcttcacc agtcacatct tctaggacct ttttgattc agttagtata agctcttcca 180
cttcctttgt taagacttca tctggtaaag tcttaagttt tgtagaaaagg aattyaattg 240
ctcgttctct aacaatgtcc tctccttgaa gtatttggct gaacaaccca cctaaagtcc 300
ctttgtgcat ccatttttaa tatacttaat agggcattgk tncactaggt taaattctgc 360
aagagtcata tgtctgcaa agttgcgtta gtatatctgc ca 402

```

```

<210> 192
<211> 601
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(601)
<223> n = A,T,C or G

```

```

<400> 192
gagctcggat ccaataatct ttgtctgagg gcagcacaca tatncagtgc catggnaact 60
ggtctacccc acatgggagc agcatgccgt agntatataa ggctattccc tgagtcagac 120
atgcytyttt gaytaccgtg tgccaagtgc tggatgattct yaacacacyt ccatcccgyt 180
cttttgtgga aaaactggca cttktctgga actagcarga catcacttac aaattcacc 240
acgagacact tgaaagggtg aacaaagcga ytcttgcatg gctttttgtc cctccggcac 300
cagttgtcaa tactaaccg ctggtttgcc tccatcacat ttgtgatctg tagctctgga 360
tacatctcct gacagtactg aagaacttct tcttttgtt caaaagcarg tcttggtgcc 420
tgttggatca gggtccatt tcccagtcyg aatgttcaca tggcatattt wacttcccac 480
aaaacattgc gatttgaggc tcagcaacag caaatcctgt tccggcattg gctgcaagag 540
cctcgatgta gccggccagc gccaaaggcag gcgccgtgag ccccaccagc agcagaagca 600
g 601

```

```

<210> 193
<211> 608
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(608)
<223> n = A,T,C or G

```

```

<400> 193
atacagccca natcccacca cgaagatgcg cttgttgact gagaacctga tgcggtcact 60
gggtccgctg tagcccccagc gactctccac ctgctggaag cggttgatgc tgcaactcytt 120
cccaacgcag gcagmagcgg gscgggtcaa tgaactccay tctgtgcttg gggtkgacgg 180
tkaagtgcag gaagaggctg accacctgcg ggtccaccag gatgcccgac tgtgcgggac 240
ctgcagcgaa actcctcgat ggatcatgagc gggaagcgaa tgaggcccag ggccttgccc 300

```

```

agaaccttcc gcctgttctc tggcgtcacc tgcagctgct gccgctgaca ctgggcctcg      360
gaccagcgga caaacggcrt tgaacagccg cacctcacgg atgcccagtg tgtcgcgctc      420
caggammgsc accagcgtgt ccaggtcaat gtcggtgaag ccctccgcgg gtrattggcg      480
ctgcagtgtt tttgtcgatg ttctccaggc acaggctggc cagctgcggg tcatcgaaga      540
gtcgcgcctg cgtgagcagc atgaaggcgt tgtcggctcg cagttcttct tcaggaactc      600
cacgcaat                                         608

```

<210> 194

<211> 392

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(392)

<223> n = A,T,C or G

<400> 194

```

gaacggctgg acctgcctc gcattgtgct tgctggcagg gaataccttg gcaagcagyt      60
ccagtcgag cagccccaga ccgctgccgc ccgaagctaa gcctgcctct ggccttcccc      120
tccgcctcaa tgcagaacca gtagtgggag cactgtgttt agagttaaga gtgaacactg      180
tttgatttta cttgggaatt tcctctgtta tatagctttt cccaatgcta atttccaaac      240
aacaacaaca aaataacatg tttgcctgtt aagttgtata aaagtaggtg attctgtatt      300
taaagaaaat attactgtta catatactgc ttgcaatttc tgtatttatt gktnctstgg      360
aaataaatat agttattaaa ggtgtgcant cc                                         392

```

<210> 195

<211> 502

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(502)

<223> n = A,T,C or G

<400> 195

```

ccsttkgagg ggtkaggkyc cagttyccga gtggaagaaa caggccagga gaagtgcgtg      60
ccgagctgag gcagatgttc ccacagtgc cccagagacc stgggstata gtytctgacc      120
cctcncaagg aaagaccacs ttctggggac atgggctgga gggcaggacc tagaggcacc      180
aagggaaggc ccattccgg ggstgttccc cgaggaggaa gggaaggggc tctgtgtgcc      240
ccccasgagg aagaggccct gagtccctgg atcagacacc ccttcacgtg tatccccaca      300
caaatgcaag ctcaccaagg tcccctctca gtccccttcc stacaccctg amcggccact      360
gscscacacc caccagagc acgccaccg ccatggggar tgtgtcaag gartcgcnng      420
gcarcgtgga catctngtcc cagaaggggg cagaatctcc aatagangga ctgarcmstt      480
gctnanaaaa aaaaaaanaaa aa                                         502

```

<210> 196

<211> 665

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(665)

<223> n = A,T,C or G

<400> 196

```

ggttacttgg tttcattgcc accacttagt ggatgtcatt tagaaccatt ttgtctgctc      60
cctctggaag ctttgcgcag agcggacttt gtaattgttg gagaataact gctgaatttt      120
wagctgtttk gagttgatts gcaccactgc acccacaact tcaatatgaa aacyawttga      180
actwatattat tatcttgtga aaagtataac aatgaaaatt ttgttcatac tgtattkac      240

```

```

aagtatgatg aaaagcaawa gatatatatt cttttattat gttaaattat gattgccatt 300
attaatcggc aaaatgtgga gtgtatgttc ttttcacagt aatatatgcc ttttgtaact 360
tcacttggtt attttattgt aaatgarta caaaattctt aatttaagar aatggtagt 420
watatttatt tcattaattt ctttcctkgt ttacgtwaat tttgaaaaga wtgcatgatt 480
tcttgacaga aatcgatctt gatgctgtgg aagtagtttg acccacatcc ctatgagttt 540
ttcttagaat gtataaagggt tgtagcccat cnaacttcaa agaaaaaaat gaccacatac 600
tttgcaatca ggctgaaatg tggcatgctn ttctaattcc aactttataa actagcaaan 660
aagtg 665

```

```

<210> 197
<211> 492
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(492)
<223> n = A,T,C or G

```

```

<400> 197
tttntttttt ttttttttgc aggaaggatt ccatttattg tggatgcatt ttcacaatat 60
atgtttattg gagcgatcca ttatcagtga aaagtatcaa gtgtttataa natttttagg 120
aaggcagatt cacagaacat gctngtcngc ttgcagtttt acctcgtana gatnacagag 180
aattatagtc naaccagtaa acnaggaatt tacttttcaa aagattaaat ccaaactgaa 240
caaaatttcta cctgaaact tactccatcc aaatattgga ataanagtca gcagtgtac 300
attctcttct gaactttaga ttttctagaa aaatatgtaa tagtgatcag gaagagctct 360
tgttcaaaag tacaacnaag caatgttccc ttaccatagg ccttaattca aactttgatc 420
catttcactc ccacacggg agtcaatgct acctgggaca cttgtatttt gttcatnctg 480
ancntggctt aa 492

```

```

<210> 198
<211> 478
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(478)
<223> n = A,T,C or G

```

```

<400> 198
tttnttttgn atttcantct gtannaanta ttttcattat gtttattana aaaatatnaa 60
tgtntccacn acaaatcatn ttacntnagt aagaggccan ctacattgta caacatacac 120
tgagtatat ttgaaaagga caagtttaaa gtanacncat attgccganc atancacatt 180
tatacatggc ttgattgata tttagcacag canaaactga gtgagttacc agaaanaaat 240
natatatgtc aatcngattt aagatacaaa acagatccta tggtagatan catcntgtag 300
gagttgtggc tttatgttta ctgaaagtca atgcagttcc tgtacaaaaga gatggccgta 360
agcattctag tacctctact ccattggttaa gaatcgtaca cttatgttta catatgtnc 420
gggtaagaat tgtgttaaagt naanttattg agagggtccan gagaaaaatt tgatncaa 478

```

```

<210> 199
<211> 482
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(482)
<223> n = A,T,C or G

```

```

<400> 199
agtgacttgt cctccaacaa aacccttga tcaagtttgt ggcaactgaca atcagaccta 60

```

```

tgctagtcc  tgcctctat  tcgctactaa  atgcagactg  gaggggacca  aaaaggggca  120
tcaactccag  ctggattatt  ttggagcctg  caaatctatt  cctacttgta  cggactttga  180
agtgattcag  tttcctctac  ggatgagaga  ctggctcaag  aatatactca  tgcagcttta  240
tgaagccnac  tctgaacacg  ctggttatct  nagatgagaa  ncagagaaat  aaagtcnaga  300
aaatttacct  ggangaaaag  aggccttngg  ctggggacca  tccattgaa  ccttctctta  360
anggacttta  agaanaaact  accacatgtn  tgtngtatcc  tgggtgccng  ccgtttantg  420
aacntngacn  ncacccttnt  ggaatanant  cttgacngcn  tctgaactt  gtcctctgc  480
ga  482

```

```

<210> 200
<211> 270
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(270)
<223> n = A,T,C or G

```

```

<400> 200
cggccgcaag  tgcaactcca  gctggggccg  tgcggacgaa  gattctgcca  gcagttggtc  60
cgactcgac  gacggcgcg  gcgacagtcg  caggtgcagc  gcgggcgcct  ggggtcttgc  120
aaggctgagc  tgacgccgca  gaggtcgtgt  cagctccac  gaccttgacg  ccgtcgggga  180
cagccggaac  agagcccggt  gaangcggga  ggctcgggg  agccctcgg  gaagggcggc  240
ccgagaata  cgcagtgca  ggtggccgca  270

```

```

<210> 201
<211> 419
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(419)
<223> n = A,T,C or G

```

```

<400> 201
ttttttttt  ttttgaatc  tactgcgagc  acagcaggtc  agcaacaagt  ttattttgca  60
gctagcaagg  taacagggtg  gggcatggtt  acatgttcag  gtcaacttcc  ttgtcgtgg  120
ttgattgggt  tgtctttatg  ggggcggggt  ggggtagggg  aaancgaagc  anaantaaca  180
tggagtgggt  gcacctccc  tgtagaacct  ggttacnaaa  gcttggggca  gttcacctgg  240
tctgtgaccg  tcattttctt  gacatcaatg  ttattagaag  tcaggatatc  ttttagagag  300
tccactgtnt  ctggagggag  attaggggtt  cttgccana  tccaancaa  atccacntga  360
aaaagtggga  tgatncangt  acngaatacc  ganggcatan  ttctcatant  cggtgcca  419

```

```

<210> 202
<211> 509
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(509)
<223> n = A,T,C or G

```

```

<400> 202
ttntttttt  ttttttttt  ttttttttt  ttttttttt  ttttttttt  ttttttttt  60
tggcacttaa  tccattttta  tttcaaaatg  tctacaaant  ttnaatncnc  cattatacng  120
gtntttttnc  aaaatctaaa  nnttatcaaa  atntnagcca  aantccttac  ncaaatnnaa  180
tacncaaaa  aatcaaaaat  atacntntct  ttcagcaaac  ttngttacat  aaattaaaaa  240
aatatatacg  gctggtgttt  tcaaagtaca  attatcttaa  cactgcaaac  atnttttnaa  300
ggaactaaaa  taataaaaaa  cactnccgca  aaggttaaag  ggaacaacaa  attcntttta  360

```



```

ttaagatcat agagcttgta agtgaaaaga taaaatttga cctcagaaac tctgagcatt      240
aaaaatccac tattagcaaa taaattacta tggacttctt gctttaattt tgtgatgaat      300
atgggggtgtc actggtaaac caacacattc tgaaggatac attacttagt gatagattct      360
tatgtacttt gctanatnac gtggatatga gttgacaagt ttctctttct tcaatctttt      420
aaggggcnga ngaaatgagg aagaaaaagaa aaggattacg catactgttc ttctatngg      480
aaggattaga tatgtttcct ttgccaatat taaaaaata ataatgttta ctactagtga      540
aacc

```

<210> 206

<211> 487

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(487)

<223> n = A,T,C or G

<400> 206

```

tttttttttt ttttttagtc aagtttctna tttttattat aattaaagtc ttggtcattt      60
catttatttag ctctgcaact tacatattta aattaaagaa acgttnttag acaactgtna      120
caatttataa atgtaagggtg ccattattga gtanataat tctccaaga gtggatgtgt      180
cccttctccc accaactaat gaancagcaa cattagttaa attttattag tagatnatac      240
actgctgcaa acgctaattc tcttctccat ccccatgtng atattgtgta tatgtgtgag      300
ttggttagaa tgcatacanca atctnacaat caacagcaag atgaagctag gcntgggctt      360
tcggtgaaaa tagactgtgt ctgtctgaat caaatgatct gacctatcct cgggtggcaag      420
aactcttcga accgcttcct caaaggcngc tgccacattt gtggcntctn ttgcacttgt      480
ttcaaaa

```

<210> 207

<211> 332

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(332)

<223> n = A,T,C or G

<400> 207

```

tgaattggct aaaagactgc atttttanaa ctagcaactc ttatttcttt cctttaaaaa      60
tacatagcat taaatcccaa atcctattta aagacctgac agcttgagaa ggctcactact      120
gcatttatag gaccttctgg tggttctgct gttacntttg aantctgaca atccttgana      180
atctttgcat gcagaggagg taaaaggat tggattttca cagaggaana acacagcgca      240
gaaatgaagg ggccaggctt actgagcttg tccactggag ggctcatggg tgggacatgg      300
aaaagaaggc agcctaggcc ctggggagcc ca

```

<210> 208

<211> 524

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(524)

<223> n = A,T,C or G

<400> 208

```

agggcggtgt gcgaggggcg ttactgtttt gtctcagtaa caataaatc aaaaagactg      60
gttggtttcc ggcccatcc aaccacgaag ttgatttctc ttgtgtgcag agtgactgat      120
tttaaaggac atggagcttg tcacaaatgtc acaatgtcac agtgtgaagg gcacactcac      180
tcccgcgtga ttcacattta gcaaccaaca atagctcatg agtccatact tgtaaatact      240

```

```

tttggcagaa tacttnttga aacttgcaga.tgataactaa gatccaagat atttcccaaa      300
gtaaatagaa gtgggtcata atattaatta cctgttcaca tcagcttcca tttacaagtc      360
atgagcccag acactgacat caaactaagc ccaacttagac tcctcaccac cagtctgtcc      420
tgtcatcaga caggaggctg tcaccttgac caaattctca ccagtcaatc atctatccaa      480
aaaccattac ctgatccact tccggtaatg caccaccttg gtga                        524

```

```

<210> 209
<211> 159
<212> DNA
<213> Homo sapien

```

```

<400> 209
gggtgaggaa atccagagtt gccatggaga aaattccagt gtcagcattc ttgtctcttg      60
tggccctctc ctacactctg gccagagata ccacagtcaa acctggagcc aaaaaggaca      120
caaaggactc tcgaccctaa ctgcccaga ccctctcca                        159

```

```

<210> 210
<211> 256
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(256)
<223> n = A,T,C or G

```

```

<400> 210
actccctggc agacaaaggc agaggagaga gctctgttag ttctgtgttg ttgaactgcc      60
actgaatttc tttccacttg gactattaca tgccanttga gggactaatg gaaaaacgta      120
tggggagatt ttanccaatt tangtntgta aatggggaga ctggggcagg cgggagagat      180
ttgcagggtg naaatgggan ggctggtttg ttanatgaac agggacatag gaggtaggca      240
ccaggatgct aatca                        256

```

```

<210> 211
<211> 264
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(264)
<223> n = A,T,C or G

```

```

<400> 211
acattgtttt tttgagataa agcattgaga gagctctcct taacgtgaca caatggaagg      60
actggaacac ataccacat ctttgttctg agggataatt ttctgataaa gtcttgctgt      120
atattcaagc acatatgtta tatattattc agttccatgt ttatagccta gttaaggaga      180
ggggagatac attcngaaag aggactgaaa gaaatactca agtnggaaaa cagaaaaaga      240
aaaaaaggag caaatgagaa gcct                        264

```

```

<210> 212
<211> 328
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

```

```

<400> 212
acccaaaaat ccaatgctga atatttggtc tcattattcc canattcttt gattgtcaaa      60

```



```

ggatttaatg ttgtctcagc ttgggcactt cagttaggac ctaaggatgc cagccggcag 120
gtttatatat gcagcaacaa tattcaagcg cgacaacagg ttattgaact tgcccggcag 180
ttnaatttca ttccattga cttgggatcc ttatcatcag ccagagagat tgaaaattta 240
cccctacnac tctttactct ctgganaggg ccagtgggtg tagctataag cttggccaca 300
tttttttttc cttttattcct ttgtcaga 328

```

<210> 213

<211> 250

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(250)

<223> n = A,T,C or G

<400> 213

```

acttatgagc agagcgacat atccnagtgt agactgaata aaactgaatt ctctccagtt 60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120
cattatgcc aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataanc catgttaana aacaaatatt tctctnacct 240
tctcatcggt 250

```

<210> 214

<211> 444

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(444)

<223> n = A,T,C or G

<400> 214

```

accagaaatc caatgctgaa tatttggtt cattattccc agattctttg attgtcaaag 60
gatttaatgt tgtctcagct tgggcacttc agttaggacc taaggatgcc agccggcagg 120
tttatatatg cagcaacaat attcaagcgc gacaacaggc tattgaactt gcccgccagt 180
tgaatttcat tcccattgac ttgggatcct tatcatcagc canagagatt gaaaatttac 240
ccctacgact ctttactctc tggagagggc cagtgggtgt agctataagc ttggccacat 300
tttttttcc tttattcctt tgtcagagat gcgattcatc catatgctan aaaccaacag 360
agtgaacttt acaaaattcc tataganatt gtgaataaaa ccttacctat agttgccatt 420
actttgctct ccctaataata cctc 444

```

<210> 215

<211> 366

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(366)

<223> n = A,T,C or G

<400> 215

```

acttatgagc agagcgacat atccaagtgt anactgaata aaactgaatt ctctccagtt 60
taaagcattg ctactgaag ggatagaagt gactgccagg agggaaagta agccaaggct 120
cattatgcc aagganatat acatttcaat tctccaaact tcttcctcat tccaagagtt 180
ttcaatattt gcatgaacct gctgataagc catgttgaga aacaaatatt tctctgacct 240
tctcatcggt aagcagaggc tgtaggcaac atggaccata gcgaanaaaa aacttagtaa 300
tccaagctgt tttctacact gtaaccagggt ttccaaccaa ggtggaaatc tcctatactt 360
ggtgcc 366

```

<210> 216
 <211> 260
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(260)
 <223> n = A,T,C or G

<400> 216
 ctgtataaac agaactccac tgcangaggg agggccgggc caggagaatc tccgcttgct 60
 caagacaggg gcctaaggag ggtctccaca ctgctnntaa gggctnttnc atttttttat 120
 taataaaaag tnnaaaaggc ctcttctcaa cttttttccc ttinggctgga aaatttataa 180
 atcaaaaatt tcctnaagtt ntcaagctat catatatact ntatcctgaa aaagcaacat 240
 aattcttcct tccctccttt 260

<210> 217
 <211> 262
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(262)
 <223> n = A,T,C or G

<400> 217
 acctacgtgg gtaagtttan aaatgttata atttcaggaa naggaacgca tataattgta 60
 tcttgccctat aattttctat tttaataagg aaatagcaaa ttgggggtggg gggaatgtag 120
 ggcattctac agtttgagca aaatgcaatt aaatgtggaa ggacagcact gaaaaatttt 180
 atgaataatc tgtatgatta tatgtctcta gagtagattt ataattagcc acttacccta 240
 atatccttca tgcttgtaaa gt 262

<210> 218
 <211> 205
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(205)
 <223> n = A,T,C or G

<400> 218
 accaaggtgg tgcattaccg gaantggatc aangacacca tcgtggccaa cccctgagca 60
 cccctatcaa ctcccttttg tagtaaaactt ggaaccttgg aaatgaccag gccaaagactc 120
 aggcctcccc agttctactg acctttgtcc ttangntna ngtccagggt tgctaggaaa 180
 anaaatcagc agacacaggt gtaaa 205

<210> 219
 <211> 114
 <212> DNA
 <213> Homo sapien

<400> 219
 tactgttttg tctcagtaac aataaatata aaaagactgg ttgtgttccg gcccacatcca 60
 accacgaagt tgatttctct tgtgtgcaga gtgactgatt ttaaaggaca tgga 114

<210> 220
 <211> 93
 <212> DNA

<213> Homo sapien

<400> 220

actagccagc acaaaaggca gggtagcctg aattgctttc tgctctttac atttctttta	60
aaataagcat ttagtgctca gtcctactg agt	93

<210> 221

<211> 167

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(167)

<223> n = A,T,C or G

<400> 221

actangtgca ggtgcgcaca aatatttgct gatattccct tcatcttgga ttccatgagg	60
tcttttgccc agcctgtggc tctactgtag taagtttctg ctgatgagga gccagnatgc	120
ccccactac ctccctgac gctcccaana aatcacccaa cctctgt	167

<210> 222

<211> 351

<212> DNA

<213> Homo sapien

<400> 222

agggcgtggt gcggagggcg gtactgacct cattagtagg aggatgcatt ctggcacccc	60
gttcttcacc tgtcccccaa tccttaaaag gccatactgc ataaagtcaa caacagataa	120
atgtttgctg aattaaagga tggatgaaaa aaattaataa tgaatttttg cataatccaa	180
ttttctcttt tatatttcta gaagaagttt ctttgagcct attagatccc gggaatcttt	240
taggtgagca tgattagaga gctttaggt tgcttttaca tatactctggc atatttgagt	300
ctcgtatcaa aacaatagat tggtaaaggt ggtattattg tattgataag t	351

<210> 223

<211> 383

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(383)

<223> n = A,T,C or G

<400> 223

aaaacaaaca aacaaaaaaa acaattcttc attcagaaaa attatcttag ggactgatat	60
tggttaattat ggtcaattta atwrttrtkt ggggcatttc cttacattgt cttgacaaga	120
ttaaaatgtc tgtgccaaaa ttttgtattt tatttgagga cttcttatca aaagtaatgc	180
tgccaaagga agtctaagga attagtagtg ttcccmccac ttgtttggag tgtgctattc	240
taaaagattt tgatttcctg gaatgacaat tatattttta ctttggtggg ggaaanagtt	300
ataggaccac agtcttcaact tctgatactt gtaaattaat cttttattgc acttgttttg	360
accattaagc tatatgttta aaa	383

<210> 224

<211> 320

<212> DNA

<213> Homo sapien

<400> 224

cccctgaagg cttcttggtta gaaaatagta cagttacaac caataggaac aacaaaaaga	60
aaaagtgtgt gacattgtag tagggagtgt gtacccttta ctccccatca aaaaaaaat	120
ggatacatgg ttaaaggata raagggaat attttatcat atgttctaaa agagaaggaa	180

gagaaaatac	tactttctcr	aaatggaagc	ccttaaaggt	gctttgatac	tgaaggacac	240
aaatgtggcc	gtccatcctc	ctttaragtt	gcatgacttg	gacacggtaa	ctgttgacgt	300
tttaractcm	gcattgtgac					320

<210> 225
 <211> 1214
 <212> DNA
 <213> Homo sapien

<400> 225						
gaggactgca	gcccgcactc	gcagccctgg	caggcggcac	tggtcatgga	aaacgaattg	60
ttctgctcgg	gcgtcctggt	gcatccgcag	tgggtgctgt	cagccgcaca	ctgtttccag	120
aactcctaca	ccatcgggct	gggcctgcac	agtcttgagg	ccgaccaaga	gccagggagc	180
cagatgggtg	aggccagcct	ctccgtacgg	caccagagat	acaacagacc	cttgctcgct	240
aacgacctca	tgctcatcaa	gttgacgaa	tccgtgtccg	agtctgacac	catccggagc	300
atcagcattg	cttcgcagtg	ccctaccgcg	gggaactctt	gcctcgtttc	tggtgggggt	360
ctgctggcga	acggcagaat	gcctaccgtg	ctgcagtgcg	tgaacgtgtc	ggtgggtgtc	420
gaggaggtct	gcagtaagct	ctatgacccg	ctgtaccacc	ccagcatgtt	ctgcgccggc	480
ggagggcaag	accagaagga	ctcctgcaac	ggtgactctg	gggggccctt	gatctgcaac	540
gggtacttgc	agggccttgt	gtctttcgga	aaagccctgt	gtggccaagt	tggtcggtcca	600
ggtgtctaca	ccaacctctg	caaattcact	gagtggatag	agaaaaccgt	ccaggccagt	660
taactctggg	gactgggaac	ccatgaaatt	gacccccaaa	tacatcctgc	ggaagggaatt	720
caggaatata	tgttcccagc	ccctcctccc	tcaggcccag	gagtccaggc	ccccagcccc	780
tcctccctca	aaaccaagggt	acagatcccc	agccctcctt	ccctcagacc	caggagtcca	840
gacccccag	cccctcctcc	ctcagaccca	ggagtccagc	ccctcctccc	tcagaccagc	900
gagtccagac	ccccagcccc	ctcctccctc	agaccagggg	gtccaggccc	ccaacccctc	960
ctccctcaga	ctcagaggtc	caagccccca	accctcctt	ccccagacc	agaggtccag	1020
gtcccagccc	ctcctccctc	agaccagcg	gtccaatgcc	acctagactc	tcctgtaca	1080
cagtggcccc	ttgtggcacg	ttgacccaac	cttaccagtt	ggtttttcat	ttttgtccc	1140
tttccctag	atccagaaat	aaagtctaag	agaagcgcaa	aaaaaaaaaa	aaaaaaaaaa	1200
aaaaaaaaaa	aaaa					1214

<210> 226
 <211> 119
 <212> DNA
 <213> Homo sapien

<400> 226						
accagtagtg	tgcagggaga	cggaacccca	tgtgacagcc	cactccacca	gggttcccaa	60
agaacctggc	ccagtcataa	tcattcatcc	tgacagtggc	aataatcacg	ataaccagt	119

<210> 227
 <211> 818
 <212> DNA
 <213> Homo sapien

<400> 227						
acaattcata	gggacgacca	atgaggacag	ggaatgaacc	cggtctctccc	ccagccctga	60
ttttgtctac	atatggggtc	ccttttcatt	ctttgcaaaa	acactggggt	ttctgagAAC	120
acggacgggt	cttagcacia	tttgtgaaat	ctgtgtaraa	ccgggctttg	caggggagat	180
aattttcctc	ctctggagga	aaggtgggtg	ttgacaggca	gggagacagt	gacaaggcta	240
gagaaagcca	cgctcggcct	tctctgaacc	aggatggaac	ggcagacccc	tgaaaacgaa	300
gcttgctccc	ttccaatcag	ccacttctga	gaacccccat	ctaacttctt	actggaaaag	360
agggcctcct	caggagcagt	ccaagagttt	tcaaagataa	cgtgacaact	accatctaga	420
ggaaaagggg	gacccctcagc	agagaagccg	agagcttaac	tctggctcgt	tccagagaca	480
acctgctggc	tgtcttgga	tgcgccagc	ctttgagagg	ccactacccc	atgaacttct	540
gccatccact	ggacatgaag	ctgaggacac	tgggcttcaa	cactgagtgt	tcatgagagg	600
gacaggtctt	gccctcaagc	cggctgaggg	cagcaaccac	tctcctcccc	tttctcacgc	660
aaagccattc	ccacaaatcc	agaccatacc	atgaagcaac	gagacccaaa	cagtttggtc	720
caagagata	tgaggactgt	ctcagcctgg	ctttgggctg	acaccatgca	cacacacaag	780
gtccacttct	aggttttcag	cctagatggg	agtcgtgt			818

<210> 228
 <211> 744
 <212> DNA
 <213> Homo sapien

<400> 228
 actggaagaca ctgttgaact tgatcaagac ccagaccacc ccaggtctcc ttcgtgggat 60
 gtcatacagc ttgacatacc tttggaacga gcctctcctc tggaagatgg aagaccgtgt 120
 tcgtggccga cctggcctct cctggcctgt ttcttaagat gcggagtcac atttcaatgg 180
 taggaaaagt ggcttcgtaa aatagaagag cagtcactgt ggaactacca aatggcgaga 240
 tgctcgggtg acattggggg gctttgggat aaaagattta tgagccaact attctctggc 300
 accagattct aggccagttt gttccactga agcttttccc acagcagtcc acctctgcag 360
 gctggcagct gaatggcttg ccggtggctc tgtggcaaga tcacactgag atcgatgggt 420
 gagaaggcta ggatgcttct ctagtgttct tagctgtcac gttggctcct tccaggttgg 480
 ccagacggtg ttggccactc ccttctaaaa cacaggcgcc ctctgtgtga cagtgacccg 540
 ccgtgggtatg ccttggccca ttccagcagt ccagttatg catttcaagt ttgggggttg 600
 ttcttttctg taatgttctc ctgtgttctc agctgtcttc atttcctggg ctaagcagca 660
 ttgggagatg tggaccagag atccactcct taagaaccag tggcgaaaaga cactttcttt 720
 cttcactctg aagtagctgg tgggt 744

<210> 229
 <211> 300
 <212> DNA
 <213> Homo sapien

<400> 229
 cgagctcggg ttttgtctat aaagtttgat ccctcctttt ctcatccaaa tcatgtgaac 60
 cattacacat cgaaataaaa gaaaggtggc agacttgccc aacgccaggc tgacatgtgc 120
 tgcagggttg ttgtttttta attattattg tttagaaacgt caccacacag cctgtttaat 180
 ttgtatgtga cagccaactc tgagaaggtc ctatttttcc acctgcagag gatccagtct 240
 cactaggctc ctctctgccc tcacactgga gtctccgcca gtgtgggtgc ccactgacat 300

<210> 230
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 230
 cagcagaaca aatacaata tgaagagtgc aaagatctca taaaatctat gctgaggaat 60
 gagcgacagt tcaaggagga gaagcttgca gagcagctca agcaagctga ggagctcagg 120
 caatataaag tcctggttca cactcaggaa cgagagctga ccaggttaag ggagaagttg 180
 cgggaaggga gagatgcctc cctctcattg aatgagcatc tccaggccct cctcactccg 240
 gatgaaccgg acaagtccca ggggcaggac ctccaagaaa cagacctcgg ccgcgaccac 300
 g 301

<210> 231
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 231
 gcaagcacgc tggcaaatct ctgtcaggtc agctccagag aagccattag tcatttttagc 60
 caggaactcc aagtcacat ccttggcaac tggggacttg cgcaggttag ccttgaggat 120
 ggcaaacacgg gacttctcat caggaagtgg gatgtagatg agctgatcaa gacggccagg 180
 tctgaggatg gcaggatcaa tgatgtcagg ccggttggtg ccgccaatga tgaacacatt 240
 tttttttgtg gacatgccat ccatttctgt caggatctgg ttgatgactc ggtcagcagc 300
 c 301

<210> 232
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 232
 agtaggtatt tcgtgagaag ttcaacacca aaactggaac atagttctcc ttcaagtgtt 60
 ggcgacagcg gggcttcctg attctggaat ataactttgt gtaaattaac agccacctat 120
 agaagagtcc atctgctgtg aaggagagac agagaactct gggttccgtc gtcctgtcca 180
 cgtgctgtac caagtgtgtg tgccagcctg ttacctgttc tcaactgaaa tctggctaata 240
 gctctgtgtg atcaactctg attctgacaa tcaatcaatc aatggcctag agcactgact 300
 g 301

<210> 233
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 233
 atgactgact tcccagtaag gctctctaag gggtaagtag gaggatccac aggatttgag 60
 atgctaaggc cccagagatc gtttgatcca accctcttat ttccagaggg gaaaatgggg 120
 cctagaagtt acagagcatc tagctggtgc gctggcacc cttggcctcac acagactccc 180
 gagtagctgg gactacaggc acacagtcac tgaagcaggc cctgttagca attctatgag 240
 tacaaattaa catgagatga gtagagactt tattgagaaa gcaagagaaa atcctatcaa 300
 c 301

<210> 234
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 234
 aggtcctaca catcgagact catccatgat tgatatgaat ttaaaaatta caagcaaaga 60
 cattttattc atcatgatgc tttcttttgt ttcttctttt cgttttcttc tttttctttt 120
 tcaatttcag caacatactt ctcaatttct tcaggattta aaatcttgag ggattgatct 180
 cgcctcatga cagcaagttc aatgtttttg ccacctgact gaaccacttc caggagtggc 240
 ttgatcacca gcttaattgt cagatcatct gcttcaatgg cttegtcagt atagttcttc 300
 t 301

<210> 235
 <211> 283
 <212> DNA
 <213> Homo sapien

<400> 235
 tggggctgtg catcaggcgg gtttgagaaa tattcaattc tcagcagaag ccagaatttg 60
 aattccctca tcttttaggg aatcatttac caggtttga gaggattcag acagctcagg 120
 tgctttcact aatgtctctg aacttctgtc cctctttgtt catggatagt ccaataaata 180
 atgttatctt tgaactgatg ctcataggag agaataaag aactctgagt gatataca 240
 ttagggattc aaagaaatat tagatttaag ctcacactgg tca 283

<210> 236
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 236
 aggtcctcca ccaactgcct gaagcacggt taaaattggg aagaagtata gtgcagcata 60
 aatactttta aatcgatcag atttccctaa cccacatgca atcttcttca ccagaagagg 120
 tcggagcagc atcattaata ccaagcagaa tgcgtaatag ataaatacaa tggatatatag 180
 tgggtagacg gcttcatgag tacagtgtac tgtggtatcg taatctggac ttgggttgta 240
 aagcatcgtg taccagtcag aaagcatcaa tactcgacat gaacgaatat aaagaacacc 300
 a 301

<210> 237
 <211> 301

<212> DNA

<213> Homo sapien

<400> 237

cagtggtagt ggtgggtggac gtggcggttg	tcgtgggtgcc ttttttgggtg cccgtcacaa	60
actcaatttt tgttcgctcc tttttggcct	tttccaattt gtccatctca attttctggg	120
ccttggctaa tgcctcatag taggagtcct	cagaccagcc atggggatca aacatatcct	180
ttgggtagtt ggtgccaagc tcgtcaatgg	cacagaatgg atcagcttct cgtaaactta	240
gggttccgaa attctttctt cctttggata	atgtagttca tatccattcc ctcctttatc	300
t		301

<210> 238

<211> 301

<212> DNA

<213> Homo sapien

<400> 238

gggcaggttt tttttttttt ttttttgatg	gtgcagaccc ttgctttatt tgtctgactt	60
gttcacagtt cagccccctg ctcaaaaaac	caacgggcca gctaaggaga ggaggaggca	120
ccttgagact tccggagtcg aggcctctcca	gggttcccca gcccatcaat cattttctgc	180
acccctgcc tgggaagcag ctccctgggg	gggtgggaatg ggtgactaga agggatttca	240
gtgtgggacc cagggtctgt tcttcacagt	aggaggtgga agggatgact aatttcttta	300
t		301

<210> 239

<211> 239

<212> DNA

<213> Homo sapien

<400> 239

ataagcagct aggggaattct ttatttagta	atgtcctaac ataaaagtgc acataactgc	60
ttctgtcaaa ccatgatact gagctttgtg	acaaccaga aataactaag agaaggcaaa	120
cataatacct tagagatcaa gaaacattta	cacagttcaa ctgtttaaaa atagctcaac	180
attcagccag tgagtagagt gtgaatgcc	gcatacacag tatacaggtc cttcaggga	239

<210> 240

<211> 300

<212> DNA

<213> Homo sapien

<400> 240

ggtcctaatag aagcagcagc ttccacattt	taacgcaggt ttacgggtgat actgtccttt	60
gggatctgcc ctccagtggg accttttaag	gaagaagtgg gcccaagcta agttccacat	120
gctgggtgag ccagatgact tctgttcctt	ggtcactttc ttcaatgggg cgaatggggg	180
ctgccaggtt tttaaaatca tgcttcatct	tgaagcacac ggtcacttca ccctcctcac	240
gctgtgggtg tactttgatg aaaataccca	ctttgttggc ctttctgaag ctataatgtc	300

<210> 241

<211> 301

<212> DNA

<213> Homo sapien

<400> 241

gaggtctggt gctgaggtct ctgggctagg	aagaggagtt ctgtggagct ggaagccaga	60
cctcttttga ggaactcca gcagctatgt	tggtgtctct gagggaatgc aacaaggctg	120
ctcctccatg tattgaaaa ctgcaactcg	gactcaactg gaagggaagt ctgctgccag	180
tgtaagaac cagcctgagg tgacagaaac	ggaagcaaac aggaacagcc agtcttttct	240
tcctcctcct gtcatacggg ctctctcaag	catcctttgt tgtcaggggc ctaaaaggga	300
g		301

<210> 242

<211> 301

```
<210> 243
<211> 301
<212> DNA
<213> Homo sapien
```

```
<210> 244
<211> 300
<212> DNA
<213> Homo sapien
```

```
<210> 245
<211> 301
<212> DNA
<213> Homo sapien
```

```
<210> 246
<211> 301
<212> DNA
<213> Homo sapien
```

<400> 246							
ggtctgtcct	acaatgcctg	cttcttgaaa	gaagtcggca	ctttctagaa	tagctaaata		60
acctggtgctt	attttaaaga	actatttgta	gctcagattg	gttttcctat	ggctaaataa		120
agtgtctctt	gtgaaaatta	ataaaaacag	tcaattcaaa	gctctgatat	atgttaccac		180
taacaatcat	actaaatata	ttttgaagta	caaagtttga	catgctctaa	agtgacaacc		240
caaatgtgtc	ttacaaaaca	cgttcctaac	aaggatatgt	ttacactacc	aatgcagaaa		300
c							301

<210> 247
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 247
 aggtcctttg gcagggtca tggatcagag ctcaaactgg agggaaaggc atttcgggta 60
 gcctaagagg gcgactggcg gcagcacaaac caaggaaggc aaggttggtt cccccacgct 120
 gtgtcctgtg ttcagggtcg acacacaatc ctcatgggaa caggatcacc catgcgctgc 180
 ccttgatgat caaggttggg gcttaagtgg attaaggag gcaagttctg gggttccttg 240
 cttttcaaac catgaagtca ggctctgtat ccctcctttt cctaactgat attctaacta 300
 a 301

<210> 248
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 248
 aggtccttgg agatgccatt tcagccgaag gactcttctw ttcggaagta caccctcact 60
 attaggaaga ttcttagggg taatttttct gaggaaggag aactagccaa cttaagaatt 120
 acaggaagaa agtggtttgg aagacagcca aagaaataaa agcagattaa attgtatcag 180
 gtacattcca gcctgttggc aactccataa aaacatttca gatttttaac ccgaatttag 240
 ctaatgagac tggatttttg ttttttatgt tgtgtgtcgc agagctaaaa actcagttcc 300
 c 301

<210> 249
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 249
 gtccagagga agcacctggg gctgaactag gcttgccctg ctgtgaactt gcacttgag 60
 ccctgacgct gctgttctcc ccgaaaaacc cgaccgacct ccgcgatctc cgtccccgcc 120
 ccagggagac acagcagtga ctcagagctg gtcgcacact gtgcctccct cctcaccgcc 180
 catcgtaatg aattattttg aaaattaatt ccaccatcct ttcagattct ggatggaaag 240
 actgaatctt tgactcagaa ttgtttgctg aaaagaatga tgtgactttc ttagtcattt 300
 a 301

<210> 250
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 250
 ggtctgtgac aaggacttgc aggctgtggg aggcaagtga cccttaacac tacacttctc 60
 cttatcttta ttggcttgat aaacataatt atttctaaca ctagcttatt tccagttgcc 120
 cataagcaca tcagtacttt tctctggctg gaatagtaaa ctaaagtatg gtacatctac 180
 ctaaaagact actatgtgga ataatacata ctaatgaagt attacatgat ttaaagacta 240
 caataaaaacc aaacatgctt ataacattaa gaaaaacaat aaagatacat gattgaaacc 300
 a 301

<210> 251
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 251
 gccgagggtcc tacatttggc ccagtttccc cctgcatcct ctccagggcc cctgcctcat 60
 agacaacctc atagagcata ggagaactgg ttgccctggg gccaggggga ctgtctggat 120
 gccaggggtc ctcaaaaatg ccactgtcac tgccaggaaa tgcttctgag cagtacacct 180
 cattgggatc aatgaaaagc ttcaagaaat cttcaggctc actctcttga aggcccgga 240

cctctggagg ggggcagtg aatcccagct ccaggacgga tcctgtcgaa aagatatacct 300
c 301

<210> 252
<211> 301
<212> DNA
<213> Homo sapien

<400> 252
gcaaccaatc actctgtttc acgtgacttt tatcaccata caatttgtgg catttcctca 60
ttttctacat tgtagaatca agagtgtaaa taaatgtata tcgatgtctt caagaatata 120
tcatttccttt ttacttagga acccattcaa aatataagtc aagaatctta atatcaacaa 180
atatatcaag caaactggaa ggcagaataa ctaccataat ttagtataag taccctaaagt 240
tttataaatc aaaagcccta atgataacca tttttagaat tcaatcatca ctgtagaatc 300
a 301

<210> 253
<211> 301
<212> DNA
<213> Homo sapien

<400> 253
ttccctaaga agatgttatt ttgttgggtt ttgttcccc tccatctcga ttctcgtacc 60
caactaaaaa aaaaaataa agaaaaaatg tgctgcgttc tgaaaaataa ctccttagct 120
tggtctgatt gttttcagac cttaaaaatat aaacttgttt cacaagcttt aatccatgtg 180
gatttttttt cttagagaac cacaaaacat aaaaggagca agtcggactg aatacctgtt 240
tccatagtgc ccacagggtta ttctcacat tttctccata ggaaaatgct ttttcccaag 300
g 301

<210> 254
<211> 301
<212> DNA
<213> Homo sapien

<400> 254
cgctgcgcct ttcccttggg ggaggggcaa ggccagaggg ggtccaagtg cagcacgagg 60
aacttgacca attcccttga agcgggtggg ttaaaccctg taaatgggaa caaatcccc 120
ccaaatctct tcatcttacc ctggtggact cctgactgta gaattttttg gttgaaacaa 180
gaaaaaaata agcctttgga cttttcaagg ttgcttaaca ggtactgaaa gactggcctc 240
acttaaaactg agccaggaaa agctgcagat ttattaatgg gtgtgttagt gtgcagtgcc 300
t 301

<210> 255
<211> 302
<212> DNA
<213> Homo sapien

<400> 255
agcttttttt tttttttttt tttttttttt ttcattaaaa aatagtgtct tttattataa 60
attactgaaa tgtttctttt ctgaatataa atataaatat gtgcaaagt tgaacttgat 120
tggtgatttg ttgagttctt caagcatctc ctaataccct caagggcctg agtagggggg 180
aggaaaaagg actggaggtg gaatctttat aaaaaacaag agtgattgag gcagattgta 240
aacattatta aaaaacaaga aacaaacaaa aaaatagaga aaaaaaccac cccaacacac 300
aa 302

<210> 256
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature

80

<222> (1)...(301)

<223> n = A,T,C or G

<400> 256

```

gttccagaaa acattgaagg tggcttccca aagtctaact agggataccc cctctagcct    60
aggacctcc  tccccacacc tcaatccacc aaaccatcca taatgcaccc agataggccc    120
acccccaaaa gcctggacac cttgagcaca cagttatgac caggacagac tcatctctat    180
aggcaaatag ctgctggcaa actggcatta cctggtttgt ggggatggg  gggcaagtgt    240
gtggcctctc ggctgggta gcaagaacat tcagggtagg cctaagttan tcgtgttagt    300
t                                                    301

```

<210> 257

<211> 301

<212> DNA

<213> Homo sapien

<400> 257

```

gttgtggagg aactctggct tgetcattaa gtectactga ttttactat cccctgaatt    60
tccccactta tttttgtctt tcaatccacc aggccttaga agaggtctac ctgcctccag    120
tcttacctag tccagtctac cccctggagt tagaatggcc atcctgaagt gaaaagtaat    180
gtcacattac tcccttcagt gatttcttgt agaagtgcc  atccctgaat gccaccaaga    240
tcttaattct cactcttta atcttatctc tttgactcct ctttacaccg gagaaggctc    300
c                                                    301

```

<210> 258

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 258

```

cagcagtagt agatgccgta tgccagcacg cccagcactc ccaggatcag caccagcacc    60
aggggccag  ccaccaggcg cagaagcaag ataaacagta ggctcaagac cagagccacc    120
cccagggcaa caagaatcca ataccaggac tgggcaaaat cttcaaagat ctttaactgt    180
atgtctcggg cattgaggct gtcaataana cgctgatccc ctgctgtatg gtggtgtcat    240
tggtgatccc tgggagcgcc ggtggagtaa cgttggtcca tggaaagcag cgcccacaac    300
t                                                    301

```

<210> 259

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 259

```

tcatatatgc aaacaaatgc agactangcc tcaggcagag actaaaggac atctcttggt    60
gtgtcctgaa gtgatttgga cccctgaggg cagacaccta agtaggaatc ccagtgggaa    120
gcaaagccat aaggaagccc aggattcctt gtgatcagga agtgggccag gaaggtctgt    180
tccagctcac atctcatctg catgcagcac ggaccggatg cgccactgg gtcttggtt    240
ccctcccatc ttctcaagca gtgtccttgt tgagccattt gcatccttgg ctccaggtgg    300
c                                                    301

```

<210> 260

<211> 301

<212> DNA

<213> Homo sapien

<400> 260

```

ttttttttct ccctaaggaa aaagaaggaa caagtctcat aaaaccaaata aagcaatggt      60
aagggtgtctt aacttgaaaa agattaggag tctactggttt acaagttata attgaatgaa      120
agaactgtaa cagccacagt tggccatttc atgccaatgg cagcaaaca caggattaac      180
tagggcaaaa taaataagtg tgtggaagcc ctgataagtg cttataaac agactgattc      240
actgagacat cagtacctgc ccgggcggcc gctcgagccg aattctgcag atatccatca      300
c                                                                                   301

```

<210> 261

<211> 301

<212> DNA

<213> Homo sapien

<400> 261

```

aaatattcga gcaaatcctg taactaatgt gtctccataa aaggctttga actcagtgaa      60
tctgcttcca tccacgattc tagcaatgac ctctcggaca tcaaagctcc tcttaagggt      120
agcaccactt attccataca attcatcagc aggaaataaa ggctcttcag aaggttcaat      180
ggtgacatcc aatttcttct gataatttag attcctcaca accttcctag ttaagtgaag      240
ggcatgatga tcatccaaag ccagtggtgc acttactcca gactttctgc aatgaagatc      300
a                                                                                   301

```

<210> 262

<211> 301

<212> DNA

<213> Homo sapien

<400> 262

```

gaggagagcc tgttacagca tttgtaagca cagaatactc caggagtatt tgtaattgtc      60
tgtgagcttc ttgcccgaag tctctcagaa atttaaaaag atgcaaatac ctgagtcacc      120
cctagacttc ctaaaccaga tcctctgggg ctggaacctg gcactctgca tttgtaatga      180
gggctttctg gtgcacacct aattttgtgc atctttgccc taaatcctgg attagtgcc      240
catcattacc cccacattat aatgggatag attcagagca gatactctcc agcaaagaat      300
c                                                                                   301

```

<210> 263

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 263

```

tttagcttgt ggtaaatgac tcacaaaact gattttaaaa tcaagttaat gtgaattttg      60
aaaattacta cttaatccta attcacaata acaatggcat taaggtttga cttgagttgg      120
ttcttagtat tatttatggt aaataggctc ttaccacttg caaataactg gccacatcat      180
taatgactga cttcccagta aggtctctta aggggtaagt angaggatcc acaggatttg      240
agatgctaag gcccagaga tcgtttgatc caacctctt attttcagag gggaaaatgg      300
g                                                                                   301

```

<210> 264

<211> 301

<212> DNA

<213> Homo sapien

<400> 264

```

aaagacgtta aaccactcta ctaccacttg tggaactctc aaagggtaaa tgacaaascc      60

```

```

aatgaatgac tctaaaaaca atatttacat ttaatggtt gtagacaata aaaaaacaag 120
gtggatagat ctagaattgt aacattttaa gaaaaccata scatttgaca gatgagaaag 180
ctcaattata gatgcaaagt tataactaaa ctactatagt agtaaagaaa tacatttcac 240
acccttcata taaattcact atcttggtt gaggcactcc ataaaatgta tcacgtgcat 300
a 301

```

```

<210> 265
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 265
tgcccaagtt atgtgtaagt gtatccgcac ccagaggtaa aactacactg tcattcttgt 60
cttctgtga cgcagtattt cttctctggg gagaagccgg gaagtcttct cctggctcta 120
catattcttg gaagtctcta atcaactttt gttccatttg ttctatttct tcaggaggga 180
ttttcagttt gtcaacatgt tctctaaca cacttgccca tttctgtaaa gaatccaaag 240
cagtccaagg ctttgacatg tcaacaacca gcataactag agtatccttc agagatacgg 300
c 301

```

```

<210> 266
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 266
taccgtctgc ctttctctcc atccaggcca tctgcgaatc tacatgggtc ctctatttcg 60
acaccagatc actctttcct ctaccacag gcttgctatg agcaagagac acaacctcct 120
ctcttctgtg ttccagcttc ttttctgtt cttcccaccc ctttaagttct attcctgggg 180
atagagacac caatacccat aacctctctc ctaagcctcc ttataacca ggggtgcacag 240
cacagactcc tgacaactgg taaggccaat gaactgggag ctcacagctg gctgtgcctg 300
a 301

```

```

<210> 267
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 267
aaagagcaca ggccagctca gcctgccctg gccatctaga ctcagcctgg ctccatgggg 60
gttctcagtg ctgagtccat ccaggaaaag ctcacctaga ctttctgagg ctgaatcttc 120
atcctcacag gcagcttctg agagcctgat attcctagcc ttgatgttct ggagtaaagc 180
ctcattctga ttctctcct tcttttctt caagtgggtt ttctctcat ccctctgttc 240
aattcgcttc agcttgctg ctttagccct catttccaga agcttcttct ctttggcatc 300
t 301

```

```

<210> 268
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 268
aatgtctcac tcaactactt ccagcctac cgtggcctaa ttctgggagt tttcttctta 60
gatcttggga gagctgggtc ttctaaggag aaggaggaag gacagatgta actttggatc 120
tcgaagagga agtctaattg aagtaattag tcaacggtcc ttgtttagac tcttggaata 180
tgctgggtgg ctcaagtggc ctttttggag aaagcaagta ttattcttaa ggagtaacca 240
cttcccattg ttctacttcc taccatcatc aattgtatat tatgtattct ttggagaact 300
a 301

```

```

<210> 269
<211> 301
<212> DNA
<213> Homo sapien

```

<400> 269
 taacaatata cactagctat ctttttaact gtccatcatt agcaccaatg aagattcaat 60
 aaaattacct ttattcacac atctcaaaac aattctgcaa attcttagtg aagtttaact 120
 atagtacacag accttaaata ttcacattgt tttctatgtc tactgaaaat aagttcacta 180
 cttttctgga tattctttac aaaatcttat taaaattcct ggtattatca ccccaatta 240
 tacagtagca caaccacctt atgtagtttt tacatgatag ctctgtagaa gtttcacatc 300
 t 301

<210> 270
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 270
 cattgaagag cttttgcgaa acatcagaac acaagtgtt ataaaattaa ttaagcctta 60
 cacaagaata catattcctt ttatttctaa ggagttaaac atagatgtag ctgatgtgga 120
 gagcttgctg gtgcagtga tattggataa cactattcat ggccgaattg atcaagtcaa 180
 ccaactcctt gaactggatc atcagaagaa ggggtgtgca cgatatactg cactagataa 240
 tggaccaacc aactaaattc tctcaccagg ctgtatcagt aaactggctt aacagaaaac 300
 a 301

<210> 271
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 271
 aaaaggttct cataagatta acaatttaaa taaatatttg atagaacatt ctttctcatt 60
 tttatagctc atcttttaggg ttgatattca gttcatgctt cccttgctgt tottgatcca 120
 gaattgcaat cacttcatca gcctgtattc gctccaattc tctataaagt ggggtccaagg 180
 tgaaccacag agccacagca cacctcttcc ccttggtgac tgccttcacc ccatganggt 240
 tctctcctcc agatganaac tgatcatgcg cccacatttt ggggttttata gaagcagtc 300
 c 301

<210> 272
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 272
 taaattgcta agccacagat aacaccaatc aaatggaaca aatcactgtc ttcaaagtgc 60
 ttatcagaaa accaaatgag cctggaatct tcataatacc taaacatgcc gtatttagga 120
 tccaataatt cctcatgat gagcaagaaa aattctttgc gcacccctcc tgcattccaca 180
 gcatcttctc caacaaatat aaccttgagt ggcttcttgt aatctatgtt ctttgttttc 240
 ctaaggactt ccattgcac tctacaata ttttctctac gcaccactag aattaagcag 300
 g 301

<210> 273
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 273
 acatgtgtgt atgtgtatct ttgggaaaaan aanaagacat cttgtttayt attttttttg 60
 agagangctg ggacatggat aatcacwtaa tttgctayta tyactttaat ctgactygaa 120
 gaaccgtcta aaaataaaaat ttaccatgtc dtatattcct tatagtatgc ttatttcacc 180
 ttttttctgt ccagagagag tatcagtgc ananatttma gggatgaamac atgmattggg 240
 gggacttnty ttacngagm accctgcccg sgcgccctcg makcngantt ccgcsananc 300
 t 301

<210> 274
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 274
 cttatatact ctttctcaga ggcaaaagag gagatgggta atgtagacaa ttctttgagg 60
 aacagtaaat gattattaga gagaangaat ggaccaagga gacagaaatt aacttgtaaa 120
 tgattctctt tggaatctga atgagatcaa gaggccagct ttagcttggtg gaaaagtcca 180
 tctaggtatg gttgcattct cgtcttcttt tctgcagtag ataagaggt aaccgaaggc 240
 aattgtgctt cttttgataa gaagctttct tggatcatatc aggaaattcc aganaaaagtc 300
 c 301

<210> 275
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 275
 tcggtgtcag cagcacgtgg cattgaacat tgcaatgtgg agcccaaacc acagaaaatg 60
 gggtgaaaatt ggccaacttt ctattaactt atgttggtgaa ttttgccacc aacagtaagc 120
 tggcccttct aataaaagaa aattgaaagg tttctcacta aacggaatta agtagtgagg 180
 tcaagagact cccaggcctc agcgtacctg cccgggcggc cgctcgaagc cgaattctgc 240
 agatatccat cacactggcg gncgctcgan catgcatcta gaaggnccaa ttcgccctat 300
 a 301

<210> 276
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 276
 tgtacacata ctcaataaat aaatgactgc attgtggtat tattactata ctgattatat 60
 ttatcatgtg acttctaatt agaaaaatgta tccaaaagca aaacagcaga tatacaaaat 120
 taaagagaca gaagatagac attaacagat aaggcaactt atacattgag aatccaaatc 180
 caatacattt aaacattttg gaaatgaggg ggacaaatgg aagccagatc aaatttgtgt 240
 aaaactattc agtatgtttc cttgtcttca tgtctgagaa ggctctcctt caatggggat 300
 g 301

<210> 277
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 277
 tttgttgatg tcagtatttt attacttgcg ttatgagtgc tcacctggga aattctaaag 60
 atacagagga cttggaggaa gcagagcaac tgaatttaat ttaaaagaag gaaaacattg 120
 gaatcatggc actcctgata ctttcccaaa tcaacactct caatgcccc ccctcgctct 180
 caccatagtg gggagactaa agtggccacg gatttgcctt angtgtgcag tgcgttctga 240
 gttcnctgtc gattacatct gaccagtctc ctttttccga agtcctccg ttcaatcttg 300
 c 301

<210> 278
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 278
 taccactaca ctccagcctg ggcaacagag caagacctgt ctcaaagcat aaaatggaat 60
 aacatatcaa atgaaacagg gaaaatgaag ctgacaattt atggaagcca gggcttgtca 120
 cagtctctac tggtattatg cattacctgg gaatttatat aagcccttaa taataatgcc 180
 aatgaacatc tcatgtgtgc tcacaatgtt ctggcactat tataagtgtc tcacaggttt 240
 tatgtgttct tcgtaacttt atggantagg tactcggccg cgaacacgct aagccgaatt 300
 c 301

<210> 279
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 279
 aaagcaggaa tgacaaagct tgcttttctg gtatgttcta ggtgtattgt gacttttact 60
 gttatattaa ttgccaatat aagtaaatat agattatata tgtatagtgt ttcacaaagc 120
 ttagaccttt acctccagc caccacacag tgcttgatat ttcagagtca gtcattgggt 180
 atacatgtgt agttccaaag cacataagct agaanaanaa atatttctag ggagcactac 240
 catctgtttt cacatgaaat gccacacaca tagaactcca acatcaattt cattgcacag 300
 a 301

<210> 280
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 280
 ggtactggag ttttctccc ctgtgaaaac gtaactactg ttgggagtga attgaggatg 60
 tagaaagggt gtggaaccaa attgtggtca atggaaatag gagaatatgg ttctcactct 120
 tgagaaaaaa acctaagatt agcccaggta gttgcctgta acttcagttt ttctgcctgg 180
 gtttgatata gtttagggtt ggggttagat taagatctaa attacatcag gacaaagaga 240
 cagactatta actccacagt taattaagga ggtatgttcc atgtttattt gttaaagcag 300
 t 301

<210> 281
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 281
 aggtacaaga aggggaatgg gaaagagctg ctgctgtggc attgttcaac ttggatattc 60
 gccgagcaat ccaaatcctg aatgaagggg catcttctga aaaaggagat ctgaatctca 120
 atgtggtagc aatggcttta tcgggttata cggtgagaa gaactccctt tggagagaaa 180
 tgtgtagcac actgcgatta cagctaaata acccgatatt gtgtgtcatg tttgcatttc 240
 tgacaagtga aacaggatct tacgatggag tttgtatga aaacaaagt gcagtacctc 300
 g 301

<210> 282
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 282
 caggctactac agaattaaaa tactgacaag caagtagttt cttggcgtgc acgaattgca 60
 tccagaaccc aaaaattaag aaattcaaaa agacattttg tgggcacctg ctagcacaga 120
 agcgagaaag caaagcccag gcagaacccat gctaacctta cagctcagcc tgcacagaag 180
 cgagaagca aagcccaggc agaaccatgc taaccttaca gctcagcctg cacagaagcg 240
 cagaagcaaa gcccaggcag aacatgctaa ccttacagct cagcctgcac agaagcacag 300
 a 301

<210> 283
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 283
 atctgtatac ggcagacaaa ctttatarag tgtagagagg tgagcgaaag gatgcaaaag 60
 cactttgagg gctttataat aatatgctgc ttgaaaaaaa aaatgtgtag ttgatactca 120
 gtgcatctcc agacatagta aggggttgct ctgaccaatc aggtgatcat tttttctatc 180
 acttcccagg ttttatgcaa aaattttggt aaattctata atggtgatat gcatctttta 240
 ggaaacatat acatttttta aaatctattt tatgtaagaa ctgacagacg aatttgcttt 300
 g 301

<210> 284
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 284
 caggtaaaaa acgctattaa gtggcttaga atttgaacat ttgtggtctt tatttacttt 60
 gcttcgtgtg tgggcaaaagc aacatcttcc ctaaatatat attaccaaga aaagcaagaa 120
 gcagattagg tttttgacaa aacaaacagg ccaaaagggg gctgacctgg agcagagcat 180
 ggtgagaggc aaggcatgag agggcaagtt tggtgtggac agatctgtgc ctactttatt 240
 actggagtaa aagaaaacaa agttcattga tgtcgaagga tatatacagt gttagaaatt 300
 a 301

<210> 285
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 285
 acatcacccat gatcggtacc cccacccatt atacgttgta tgtttacata aatactcttc 60
 aatgatcatt agtgttttaa aaaaaatact gaaaactcct tctgcatccc aatctctaac 120
 caggaaagca aatgctatct acagacctgc aagccctccc tcaaacnaaa ctatttctgg 180
 attaaatagc tctgacttct tttgaggtca cactgactagg caaatgctat ttacgatctg 240
 caaaagctgt ttgaagagtc aaagccccc a ttttctggac cctgtaacag 300
 t 301

<210> 286
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 286
 taccactgca ttccagcctg ggtgacagag tgagactccg tctccaaaaa aaactttgct 60
 tgtatattat ttttgcctta cagtggatca ttctagtagg aaaggacagt aagatttttt 120
 atcaaaatgt gtcagtcagg taagagatgt tatattcttt tctcatttct tccccacca 180
 aaaataagct accatatagc ttataagctc caaatttttg ctttttacta aaatgtgatt 240
 gtttctgttc attgtgtatg cttcatcacc tatattagga aaattccatt ttttcccttg 300
 t 301

<210> 287
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 287
 tacagatctg ggaactaaat attaaaaatg agtgtggctg gatatatgga gaatgttggg 60
 ccagaaagga acgtagagat cagatattac aacagctttg ttttgagggt tagaaatatg 120
 aaatgatctg gttatgaacg cacagttagg gcagcagggc cagaatcctg accctctgcc 180
 ccgtgggtat ctctcccca gcttggctgc ctcatgttat cacagtattc cattttgttt 240
 gttgcatgtc ttgtgaagcc atcaagatct tctcgtctgt tttcctctca ttggtaatgc 300
 t 301

<210> 288
 <211> 301
 <212> DNA
 <213> Homo sapien

<400> 288
 gtacaccta ctgcaaggac agctgaggaa tgtaatgggc agccgctttt aaagaagtag 60
 agtcaatagg aagacaaatt ccagttccag ctcatctctg gtatctgcaa agctgcaaaa 120
 gatcttttaa gacaatttca agagaatatt tccttaaaagt tggcaatttg gagatcatac 180
 aaaagcatct gcttttgtga tttaatttag ctcatctggc cactggaaga atccaaacag 240
 tctgccttaa ttttgatga atgcatgatg gaaattcaat aatttagaaa gttaaaaaaa 300
 a 301

<210> 289
 <211> 301
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(301)
 <223> n = A,T,C or G

<400> 289
 ggtacactgt ttccatgta tgtttctaca cattgctacc tcagtgtcc tggaaactta 60
 gcttttgatg tctccaagta gtccacctc atttaactct ttgaaactgt atcatctttg 120
 ccaagtaaga gtggtggcct atttcagctg ctttgacaaa atgactggct cctgacttaa 180

```

cgttctataa atgaatgtgc tgaagcaaag tgcccatggt ggcggcgaan aagagaaaaga    240
tgtgttttgt tttggactct ctgtgggtccc ttccaatgct gtgggtttcc aaccagnnga    300
a                                                                    301

```

```

<210> 290
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 290
acactgagct cttcttgata aatatacaga atgcttggca tatacaagat tctatactac    60
tgactgatct gttcatttct ctcacagctc ttaccccca aagcttttcc accctaagtg    120
ttctgacctc cttttctaata cacagtaggg atagaggcag anccacctac aatgaacatg    180
gagtcttctc aagaggcaga aacagcacag aatcccagtt ttaccattcg ctagcagtgc    240
tgccctgaac aaaaacattt ctccatgtct cattttcttc atgcctcaag taacagtgcg    300
a                                                                    301

```

```

<210> 291
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 291
caggtaccaa tttcttctat cctagaaaca tttcatttta tgttggtgaa acataacaac    60
tatatacagct agattttttt tctatgcttt acctgctatg gaaaatttga cacattctgc    120
tttactcttt tgtttatagg tgaatcacia aatgtatttt tatgtattct gtagttcaat    180
agccatggct gtttacttca tttaatttat ttagcataaa gacattatga aaaggcctaa    240
acatgagctt cacttcccca ctaactaatt agcatctggt atttcttaac cgtaatgcct    300
a                                                                    301

```

```

<210> 292
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 292
accttttagt agtaatgtct aataataaat aagaaatcaa ttttataagg tccatatagc    60
tgtattaaat aattttttaag tttaaaagat aaaataccat catttttaaat gttggtattc    120
aaaaccaaag natataaccg aaaggaaaaa cagatgagac ataaaaatgat ttgcnagatg    180
ggaaatatag tasttyatga atgttnatta aattccagtt ataatagtgg ctacacactc    240
tcactacaca cacagacccc acagtcctat atgccacaaa cacatttcca taacttgaaa    300
a                                                                    301

```

```

<210> 293
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 293
ggtaccaagt gctgtgtgcc gctgtgtacc tgttctcact gaaaagtctg gctaattgctc    60
ttgtgtagtc acttctgatt ctgacaatca atcaatcaat ggccctagagc actgactggt    120
aacacaaacg tcactagcaa agtagcaaca gctttaagtc taaatacaaa gctgttctgt    180

```

```

gtgagaatTT tttaaaaggc tacttgata ataacccttg tcatttttaa tgtacctggg      240
ccgcgaccac gctaagccga attctgcaga tatccatcac actggcggcc gctcgagcat      300
g                                                                           301

```

```

<210> 294
<211> 301
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

```

```

<400> 294
tgacccataa caatatacac tagctatctt tttaaactgtc catcattagc accaatgaag      60
attcaataaaa attaccttta ttcacacatc tcaaaaacaat tctgcaaatt cttagtgaag      120
tttaactata gtcacaganc ttaaataattc acattgtttt ctatgtctac tgaaaaataag      180
ttcactactt ttctgggata ttctttacaa aatcttatta aaattcctgg tattatcacc      240
cccaattata cagtagcaca accaccttat gtagttttta catgatagtc ctgtagaggt      300
t                                                                           301

```

```

<210> 295
<211> 305
<212> DNA
<213> Homo sapien

```

```

<400> 295
gtactctttc tctcccctcc tctgaattta attctttcaa cttgcaattt gcaaggatta      60
cacatttcac tgtgatgtat attgtgttgc aaaaaaaaaa gtgtctttgt ttaaaattac      120
ttggtttgat aatccatctt gctttttccc cattggaact agtcattaac ccatctctga      180
actggtagaa aaacrtctga agagctagtc tatcagcatc tgacaggtga attggatggt      240
tctcagaacc atttcacca gacagcctgt ttctatcctg ttttaataaat tagtttgggt      300
tctct                                                                           305

```

```

<210> 296
<211> 301
<212> DNA
<213> Homo sapien

```

```

<400> 296
aggtagctatg ggaagctgct aaaataatat ttgatagtaa aagtagtaa tgtgctatct      60
cacctagtag taaactaaaa ataaactgaa actttatgga atctgaagtt attttccttg      120
attaaataga attaataaac caatatgagg aaacatgaaa ccatgcaatc tactatcaac      180
tttgaaaaag tgattgaacg aaccacttag ctttcagatg atgaacactg ataagtcatt      240
tgtcattact ataaatttta aaatctgtta ataagatggc ctatagggag gaaaaagggg      300
c                                                                           301

```

```

<210> 297
<211> 300
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(300)
<223> n = A,T,C or G

```

```

<400> 297
actgagtttt aactggagcg caagcaggca aggtggaag gttttgctct ctttgtgcta      60
aagggttttg aaaccttgaa ggagaatcat ttgacaaga agtacttaag agtctagaga      120
acaaagangt gaaccagctg aaagctctcg ggggaanctt acatgtgttg ttaggcctgt      180

```

tccatcattg ggagtgcact ggccatccct caaaatttgt ctgggctggc ctgagtggtc 240
accgcacctc ggccgcgacc acgctaagcc gaattctgca gatatccatc acactggcgg 300

<210> 298
<211> 301
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(301)
<223> n = A,T,C or G

<400> 298
tatggggttt gtcacccaaa agctgatgct gagaaaggcc tccctggggc ccctcccgcg 60
ggcatctgag agacctgggtg ttccagtgtt tctggaaatg ggtcccagtg ccgccggctg 120
tgaagctctc agatcaatca cgggaagggc ctggcggtgg tggccacctg gaaccaccct 180
gtcctgtctg ttacatttc actaycaggt tttctctggg cattacnatt tgttccccta 240
caacagtgac ctgtgcattc tgctgtggcc tgctgtgtct gcaggtggct ctcagcgagg 300
t 301

<210> 299
<211> 301
<212> DNA
<213> Homo sapien

<400> 299
gttttgagac ggagtttcac tcttgttgcc cagactggac tgcaatggca gggctctctgc 60
tcaactgcacc ctctgcctcc caggttcgag caattctcct gcctcagcct cccaggtagc 120
tggtattgca ggctcacgcc accataccca gctaattttt ttgtattttt agtagagacg 180
gagtttcgcc atgttggcca gctggtctca aactcctgac ctcaagcgac ctgcctgcct 240
cggcctccca aagtgtcgga attataggca tgagtcaaca cgcccagcct aaagatatatt 300
t 301

<210> 300
<211> 301
<212> DNA
<213> Homo sapien

<400> 300
attcagtttt atttgctgcc ccagtatctg taaccaggag tgccacaaaa tcttgccaga 60
tatgtcccac acccactggg aaaggctccc acctggctac ttcctctatc agctgggtca 120
gctgcattcc acaagggttct cagcctaatt agtttacta cctgcccagtc tcaaaactta 180
gtaaagcaag accatgacat tccccacgg aaatcagagt ttgccccacc gtcttgttac 240
tataaagcct gcctctaaca gtccttgctt cttcacacca atcccagagc catcccccat 300
g 301

<210> 301
<211> 301
<212> DNA
<213> Homo sapien

<400> 301
ttaaattttt gagaggataa aaaggacaaa taatctagaa atgtgtcttc ttcagtctgc 60
agaggacccc aggtctccaa gcaaccacat ggtcaagggc atgaataatt aaaagtggg 120
gggaactcac aaagaccctc agagctgaga caccacacac agtgggagct cacaaagacc 180
ctcagagctg agacaccac aacagtggga gtcacaaaag accctcagag ctgagacacc 240
cacacagca cctcggttcag ctgccacatg tgtgaataag gatgcaatgt ccagaagtgt 300
t 301

<210> 302
<211> 301

<212> DNA

<213> Homo sapien

<400> 302

```

aggtacacat ttagcttgtg gtaaatgact cacaaaactg attttaaaat caagttaatg      60
tgaattttga aaattactac ttaatcctaa ttcacaataa caatggcatt aaggtttgac      120
ttgagttggt tcttagtatt atttatggta aataggctct taccacttgc aaataactgg      180
ccacatcatt aatgactgac ttcccagtaa ggctctctaa ggggtaagta ggaggatcca      240
caggatttga gatgctaagg ccccagagat cgtttgatcc aaccctctta ttttcagagg      300
g                                                                                   301

```

<210> 303

<211> 301

<212> DNA

<213> Homo sapien

<400> 303

```

aggtaccaac tgtggaaata ggtagaggat cattttttct ttccatatca actaagttgt      60
atattgtttt ttgacagttt aacacatctt cttctgtcag agattctttc acaatagcac      120
tggctaattg aactaccgct tgcattgtta aaatgggtgg ttgtgaaatg atcataggcc      180
agtaacgggt atgtttttct aactgatctt ttgctcgttc caaagggacc tcaagacttc      240
catcgatttt atatctgggg tctagaaaag gagttaatct gttttccctc ataaattcac      300
c                                                                                   301

```

<210> 304

<211> 301

<212> DNA

<213> Homo sapien

<400> 304

```

acatggatgt tatttttcag actgtcaacc tgaatttgta tttgcttgac attgcctaatt      60
tattagtttc agtttcagct taccactttt ttgtctgcaa catgcaraas agacagtgcc      120
cttttttagtg tatcatatca ggaatcatct cacattggtt tgtgccatta ctggtgcagt      180
gactttcagc cacttgggta aggtggagtt ggccatatgt ctccactgca aaattactga      240
ttttcctttt gtaattaata agtgtgtgtg tgaagattct ttgagatgag gtatatatct      300
c                                                                                   301

```

<210> 305

<211> 301

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(301)

<223> n = A,T,C or G

<400> 305

```

gangtacagc gtggtcaagg taacaagaag aaaaaaatgt gagtggcatc ctgggatgag      60
caggggggaca gacctggaca gacacgttgt catttgctgc tgtgggtagg aaaatgggcg      120
taaaggagga gaaacagata caaatctccc aactcagtat taaggtattc tcatgcctag      180
aatattggta gaaacaagaa tacattcata tggcaataa ctaaccatgg tggaacaaaa      240
ttctgggatt taagttggat accaangaaa ttgtattaaa agagctgttc atggaataag      300
a                                                                                   301

```

<210> 306

<211> 8

<212> PRT

<213> Homo sapien

<400> 306

Val Leu Gly Trp Val Ala Glu Leu

1 5

<210> 307
 <211> 637
 <212> DNA
 <213> Homo sapien

<400> 307

acaggggratg	aagggaaagg	gagaggatga	ggaagccccc	ctggggattt	ggtttggtcc	60
ttgtgatcag	gtgggtctatg	gggcttatcc	ctacaaagaa	gaatccagaa	ataggggcac	120
attgaggaat	gatacttgag	cccaaagagc	attcaatcat	tgttttattt	gccttmtttt	180
cacaccattg	gtgaggagg	gattaccacc	ctggggttat	gaagatgggt	gaacacccca	240
cacatagcac	cggagatatg	agatcaacag	tttcttagcc	atagagattc	acagcccaga	300
gcaggaggac	gcttgccacac	catgcaggat	gacatggggg	atgcgctcgg	gattggtgtg	360
aagaagcaag	gactgttaga	ggcaggcttt	atagtaacaa	gacggtgggg	caaactctga	420
tttccgtggg	ggaatgtcat	ggctctgctt	tactaagttt	tgagactggc	aggtagttaa	480
actcattagg	ctgagaacct	tgtggaatgc	acttgacca	sctgatagag	gaagtagcca	540
ggtgggagcc	tttcccagtg	ggtgtgggac	atatctggca	agattttgtg	gcactcctgg	600
ttacagatac	tggggcagca	aataaaaactg	aatcttg			637

<210> 308
 <211> 647
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(647)
 <223> n = A,T,C or G

<400> 308

acgattttca	ttatcatgta	aatcgggtca	ctcaaggggc	caaccacagc	tgggagccac	60
tgctcagggg	aaggttcata	tgggactttc	tactgcccaa	ggttctatac	aggatataaa	120
ggngcctcac	agtatagatc	tggtagcaaa	gaagaagaaa	caaacactga	tctctttctg	180
ccaccctct	gaccctttgg	aactcctctg	accctttaga	acaagcctac	ctaatactcg	240
ctagagaaaa	gaccaacaac	ggcctcaaag	gatctcttac	catgaaggtc	tcagctaatt	300
cttggctaag	atgtgggttc	cacattaggt	tctgaatatg	gggggaaggg	tcaatttgct	360
cattttgtgt	gtggataaag	tcaggatgcc	caggggccag	agcagggggc	tgcttgcttt	420
gggaacaatg	gctgagcata	taaccatagg	ttatggggaa	caaaacaaca	tcaaagtcac	480
tgatatcaatt	gccatgaaga	cttgagggac	ctgaatctac	cgattcatct	taaggcagca	540
ggaccagttt	gagtggcaac	aatgcagcag	cagaatcaat	ggaaacaaca	gaatgattgc	600
aatgtccttt	ttttctcct	gcttctgact	tgataaaagg	ggaccgt		647

<210> 309
 <211> 460
 <212> DNA
 <213> Homo sapien

<400> 309

actttatagt	ttaggctgga	cattggaaaa	aaaaaaaaagc	cagaacaaca	tgtgatagat	60
aatatgattg	gctgcacact	tccagactga	tgaatgatga	acgtgatgga	ctattgtatg	120
gagcacatct	tcagcaagag	ggggaataac	tcatcatttt	tggccagcag	ttgtttgatc	180
accaaacatc	atgccagaat	actcagcaaa	ccttcttagc	tcttgagaag	tcaaagtccg	240
ggggaattta	ttcctggcaa	ttttaattgg	actccttatg	tgagagcagc	ggctaccag	300
ctgggggtgg	ggagcgaacc	cgtcactagt	ggacatgcag	tggcagagct	cctggttaacc	360
acctagagga	atacacaggc	acatgtgtga	tgccaagcgt	gacacctgta	gcactcaaatt	420
ttgtcttggt	tttgtctttc	ggtgtgtaag	attcttaagt			460

<210> 310
 <211> 539
 <212> DNA
 <213> Homo sapien

<400> 310

acgggactta	tcaaataaag	ataggaaaag	aagaaaactc	aaatattata	ggcagaaatg	60
ctaaaggttt	taaaatatgt	caggattgga	agaaggcatg	gataaagaac	aaagttcagt	120
taggaagag	aaacacagaa	ggaagagaca	caataaaagt	cattatgtat	tctgtgagaa	180
gtcagacagt	aagatttggt	ggaaatgggt	tggtttgttg	tatggtatgt	attttagcaa	240
taatctttat	ggcagagaaa	gctaaaatcc	tttagcttgc	gtgaatgatc	acttgctgaa	300
ttcctcaagg	taggcatgat	gaaggagggt	ttagaggaga	cacagacaca	atgaactgac	360
ctagatagaa	agccttagta	tactcagcta	ggaatagtga	ttctgagggc	acactgtgac	420
atgattatgt	cattacatgt	atggtagtga	tgggagatga	aggaaggaag	aacttatggc	480
atattttcac	ccccacaaaa	gtcagttaaa	tattgggaca	ctaaccatcc	aggtcaaga	539

<210> 311

<211> 526

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(526)

<223> n = A,T,C or G

<400> 311

caaatttgag	ccaatgacat	agaattttac	aaatcaagaa	gcttattctg	gggccatttc	60
ttttgacgtt	ttctctaaac	tactaaagag	gcattaatga	tccataaatt	atattatcta	120
catttacagc	atttaaaatg	tggtcagcat	gaaatattag	ctacagggga	agctaaataa	180
attaaacatg	gaataaagat	ttgtccttaa	atataatcta	caagaagact	ttgatatttg	240
tttttcacaa	gtgaagcatt	cttataaagt	gtcataacct	ttttggggaa	actatgggaa	300
aaaaatgggga	aactctgaag	ggtttttaagt	atcttacctg	aagctacaga	ctccataaacc	360
tctctttaca	gggagctcct	gcagccccta	cagaaatgag	tggtctgagat	tcttgatgac	420
acagcaagag	cttctcatct	aaaccctttc	cctttttagt	atctgtgtat	caagtataaa	480
agttctataa	actgtagtnt	acttatttta	atccccaaag	cacagt		526

<210> 312

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 312

cctctctctc	cccaccccct	gactctagag	aactgggttt	tctcccagta	ctccagcaat	60
tcattttctga	aagcagttga	gccactttat	tccaaagtac	actgcagatg	ttcaaactct	120
ccattttctct	ttcccttcca	cctgccagtt	ttgctgactc	tcaacttgtc	atgagtgtaa	180
gcattaagga	cattatgctt	cttcgattct	gaagacaggc	cctgctcatg	gatgactctg	240
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tgcatgatgc	tagcagcttc	agacatttgg	ttaagaacct	atgggaaaaa	aaaaaatcct	360
tgtaaatgtg	gtttcctttg	ttaaccanga	ttcttatttg	nctggtatag	aatatcagct	420
ctgaacgtgt	ggtaaagatt	tttgtgtttg	aatataggag	aatcagttt	gctgaaaagt	480
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<210> 313

<211> 718

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(718)

<223> n = A,T,C or G

<400> 313

ggagatttgt	gtggtttgca	gccgagggag	accaggaaga	tctgcatggt	gggaaggacc	60
tgatgataca	gaggtgagaa	ataagaaagg	ctgctgactt	taccatctga	ggccacacat	120
ctgctgaaat	ggagataatt	aacatcacta	gaaacagcaa	gatgacaata	taatgtctaa	180
gtagtgacat	gtttttgcac	atttccagcc	cttttaaata	tccacacaca	caggaagcac	240
aaaaggaagc	acagagatcc	ctgggagaaa	tgcccggccg	ccatcttggg	tcatcgatga	300
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cttgatggtt	cacaagacat	gcaacaaaca	aaatggaata	ctgtgatgac	acgagcagcc	540
aactggggag	gagataccac	ggggcagagg	tcaggattct	ggccctgctg	cctaactgtg	600
cgttatacca	atcatttcta	tttctaccct	caaacaagct	gtngaatatc	tgacttacgg	660
ttctnttggc	ccacattttc	atnatccacc	ccntcntttt	aannttantc	caaantgt	718

<210> 314

<211> 358

<212> DNA

<213> Homo sapien

<400> 314

gtttattttac	attacagaaa	aaacatcaag	acaatgtata	ctatttcaaa	tatatccata	60
cataatcaaa	tatagctgta	gtacatgttt	tcattgggtg	agattaccac	aaatgcaagg	120
caacatgtgt	agatctcttg	tcttattctt	ttgtctataa	tactgtattg	tgtagtccaa	180
gctctcggtg	gtccagccac	tgtgaaacat	gctcccttta	gattaacctc	gtggacgctc	240
ttgttgatt	gctgaactgt	agtgccctgt	atthttgctt	tgtctgtgaa	ttctgttgct	300
tctggggcat	ttccttgtga	tgacagaggac	caccacacag	atgacagcaa	tctgaatt	358

<210> 315

<211> 341

<212> DNA

<213> Homo sapien

<400> 315

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ataggtgatg	atgaggacat	ggaatggggc	cccaaggatg	gtctgtccaa	agaagcgagt	120
gacccccatt	ctgaagatgt	ctggaacctc	taccagcagg	atgatgatag	ccccaatgac	180
agtcaccagc	tccccgacca	gccggatatc	gtccttaggg	gtcatgtagg	cttcctgaag	240
tagcttctgc	tgtaagaggg	tggtgtcccg	ggggctcgtg	cggttattgg	tcctgggctt	300
gagggggcgg	tagatgcagc	acatggtgaa	gcagatgatg	t		341

<210> 316

<211> 151

<212> DNA

<213> Homo sapien

<400> 316

agactgggca	agactcttac	gccccacact	gcaatttggt	cttggtgccg	tatccattta	60
tgtgggcctt	tctcgagttt	ctgattataa	acaccactgg	agcgatgtgt	tgactggact	120
cattcaggga	gctctgggtg	caatattagt	t			151

<210> 317

<211> 151

<212> DNA

<213> Homo sapien

<400> 317

agaactagtg	gatcctaata	aaataacctga	aacatatatt	ggcattttatc	aatggctcaa	60
atcttcattt	atctctggcc	ttaaacctgg	ctcctgaggc	tgcggccagc	agatcccagg	120
ccagggctct	gttcttgcca	cacctgcttg	a			151

<210> 318
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 318
 actggtggga ggcgctgttt agttggctgt tttcagaggg gtctttcgga gggacctcct 60
 gctgcaggct ggagtgtctt tattcctggc gggagaccgc acattccact gctgaggctg 120
 tgggggcggt ttatcaggca gtgataaaca t 151

<210> 319
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 319
 aactagtga tccagagcta taggtacagt gtgatctcag ctttgcaaac acattttcta 60
 catagatagt actaggtatt aatagatatg taaagaaaga aatcacacca ttaataatgg 120
 taagattggg tttatgtgat tttagtggg a 151

<210> 320
 <211> 150
 <212> DNA
 <213> Homo sapien

<400> 320
 aactagtga tccactagtc cagtgtgggt gaattccatt gtgttggggt tctagatcgc 60
 gagcggtgc cttttttttt tttttttttg ggggggaatt tttttttttt aatagttatt 120
 gagtgttcta cagcttacag taaataccat 150

<210> 321
 <211> 151
 <212> DNA
 <213> Homo sapien

<400> 321
 agcaactttg tttttcatcc aggttatattt aggccttagga tttcctctca cactgcagtt 60
 taggggtggca ttgtaaccag ctatggcata ggtgttaacc aaaggctgag taaacatggg 120
 tgcctctgag aaatcaaagt cttcatacac t 151

<210> 322
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature
 <222> (1)...(151)
 <223> n = A,T,C or G

<400> 322
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 tttgggcttg gtcagtttgc cacagggtt ggagatgggt acagtcttct ggcattcggc 120
 attgtgcagg gctcgttca nacttcagtt t 151

<210> 323
 <211> 151
 <212> DNA
 <213> Homo sapien

<220>
 <221> misc_feature

<222> (1)...(151)

<223> n = A,T,C or G

<400> 323

tgaggacttg	tkttttttt	ctttattttt	aatcctctta	ckttgtaaat	atattgccta	60
nagactcant	tactaccag	tttgtggtt	twtgaggagaa	atgtaactgg	acagttagct	120
gttcaatyaa	aaagacactt	ancccatgtg	g			151

<210> 324

<211> 461

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(461)

<223> n = A,T,C or G

<400> 324

acctgtgttg	aatttcagct	ttcctcatgc	aaaaggattt	tgtatccccg	gcctacttga	60
agaagtgtc	agctaaagga	atccaggttg	ttggttgac	tgtaataacc	tttcatgaaa	120
agagttacta	cgaatcccat	cttggttcca	gctatatcac	tgacagcatg	gtagaagact	180
gcgaacctca	cttctagact	ttcacggttg	gacgaaacgg	gttcagaaac	tgccaggggc	240
ctcatacagg	gatatacaaa	taccctttgt	gctaccagg	ccctggggaa	tcaggtgact	300
cacacaaatg	caatagtgtg	tcaactgcatt	tttacctgaa	ccaaagctaa	acccggtgtt	360
gccaccatgc	accatggcat	gccagagttc	aacactgttg	ctcttgaaaa	ttgggtctga	420
aaaaacgcac	aagagcccct	gccctgccct	agctgangca	c		461

<210> 325

<211> 400

<212> DNA

<213> Homo sapien

<400> 325

acactgtttc	catgttatgt	ttctacacat	tgtacctca	gtgctcctgg	aaacttagct	60
tttcatgtct	ccaagtagtc	caccttcatt	taactctttg	aaactgtatc	atctttgcc	120
agtaagagtg	gtggcctatt	tcagctgctt	tgacaaaatg	actggctcct	gacttaacgt	180
tctataaatg	aatgtgctga	agcaaaagtc	ccatggtggc	ggcgaagaag	agaaagatgt	240
gttttgtttt	ggactctctg	tggtcccttc	caatgctgtg	ggtttccaac	caggggaagg	300
gtcccttttg	cattgccaaag	tgccataacc	atgagcacta	cgctaccatg	gttctgcctc	360
ctggccaagc	aggctggttt	gcaagaatga	aatgaatgat			400

<210> 326

<211> 1215

<212> DNA

<213> Homo sapien

<400> 326

ggaggactgc	agcccgact	cgcagccctg	gcaggcgga	ctggctcatg	aaaacgaatt	60
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gaactcctac	accatcgggc	tgggcctgca	cagtcttgag	gccgaccaag	agccagggag	180
ccagatggtg	gaggccagcc	tctccgtacg	gcacccagag	tacaacagac	ccttgctcgc	240
taacgacctc	atgctcatca	agttggacga	atccgtgtcc	gagtctgaca	ccatccggag	300
catcagcatt	gcttcgcagt	gccctaccgc	ggggaaactct	tgctcgtttt	ctggctgggg	360
tctgctggcg	aacggcagaa	tgccctaccgt	gctgcagtgc	gtgaacgtgt	cgggtggtgc	420
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cggaggggcaa	gaccagaagg	actcctgcaa	cgggtgactct	ggggggcccc	tgatctgcaa	540
cgggtacttg	cagggccttg	tgtctttcgg	aaaagccccg	tgtggccaag	ttggcgtgcc	600
aggtgtctac	accaacctct	gcaaattcac	tgagtggata	gagaaaaacc	tccaggccag	660
ttactcttgg	ggactgggaa	cccatgaaat	tgacccccaa	atacatcctg	cgggaaggat	720
tcagggaatat	ctgttcccag	cccctcctcc	ctcaggccca	ggagtccagg	ccccagccc	780
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```

agacccccca gccctctctc cctcagaccc aggagtccag cccctctctc ctcagaccca 900
ggagtccaga cccccagcc cctcctccct cagacccagg ggtccaggcc cccaaccct 960
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acagtgcgcc cttgtggcac gttgacccaa ccttaccagt tggtttttca tttttgtcc 1140
ctttcccta gatccagaaa taaagtctaa gagaagcgca aaaaaaaaa aaaaaaaaa 1200
aaaaaaaaa aaaaa 1215

```

<210> 327
 <211> 220
 <212> PRT
 <213> Homo sapien

```

<400> 327
Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 1          5          10          15
Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
          20          25          30
Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
          35          40          45
Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
          50          55          60
Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
          65          70          75          80
Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
          85          90          95
Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
          100          105          110
Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
          115          120          125
Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
          130          135          140
Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
          145          150          155          160
Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
          165          170          175
Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
          180          185          190
Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
          195          200          205
Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser
          210          215          220

```

<210> 328
 <211> 234
 <212> DNA
 <213> Homo sapien

```

<400> 328
cgctcgtctc tggtagctgc agccaaatca taaacggcga ggactgcagc ccgcactcgc 60
agccctggca ggcggcactg gtcattgaaa acgaattgtt ctgctcgggc gtccctggtgc 120
atccgcagtg ggtgctgtca gccacacact gtttcagaa ctcctacacc atcgggctgg 180
gcctgcacag tcttgaggcc gaccaagagc cagggagcca gatggtggag gcca 234

```

<210> 329
 <211> 77
 <212> PRT
 <213> Homo sapien

```

<400> 329
Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly Glu Asp Cys Ser
 1          5          10          15

```

Pro	His	Ser	Gln	Pro	Trp	Gln	Ala	Ala	Leu	Val	Met	Glu	Asn	Glu	Leu
			20					25					30		
Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp	Val	Leu	Ser	Ala	Thr
		35					40					45			
His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu	Gly	Leu	His	Ser	Leu
		50				55					60				
Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val	Glu	Ala			
65					70					75					

```
<210> 330
<211> 70
<212> DNA
<213> Homo sapien
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<400> 330
cccaacacaa tggcccgatc ccatccctga ctccgccctc aggatcgctc gtctctggta 60
gctgcagcca 70

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<210> 331
<211> 22
<212> PRT
<213> Homo sapien
```

<400> 331
Gln His Asn Gly Pro Ile Pro Ser Leu Thr Pro Pro Ser Gly Ser Leu
1 5 10 15
Val Ser Gly Ser Cys Ser
20

```
<210> 332
<211> 2507
<212> DNA
<213> Homo sapien
```

<400> 332								
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<210> 333

<211> 3030

<212> DNA

<213> Homo sapien

<400> 333

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gctccatgga	gcccggaat	tatgccacct	tggtggagc	caaggatata	gaaggcttgc	180
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<211> 2417

<212> DNA

<213> Homo sapien

<400> 334

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<210> 335

<211> 2984

<212> DNA

<213> Homo sapien

<400> 335

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<210> 336

<211> 147

<212> PRT

<213> Homo sapien

<400> 336

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102

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Pro Lys Gln Pro Gln Lys Arg Ser Arg Ala Ala Phe Ser His Thr Gln
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Val Ile Glu Leu Glu Arg Lys Phe Ser His Gln Lys Tyr Leu Ser Ala
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Pro Glu Arg Ala His Leu Ala Lys Asn Leu Lys Leu Thr Glu Thr Gln
65                70                75                80
Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys Thr Lys Arg Lys Gln
                85                90                95
Leu Ser Ser Glu Leu Gly Asp Leu Glu Lys His Ser Ser Leu Pro Ala
                100                105                110
Leu Lys Glu Glu Ala Phe Ser Arg Ala Ser Leu Val Ser Val Tyr Asn
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Ala Phe Trp
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<210> 337
<211> 9
<212> PRT
<213> Homo sapien

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<210> 338
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<212> PRT
<213> Homo sapien

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<210> 339
<211> 318
<212> PRT
<213> Homo sapien

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Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly
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50                55                60
Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu
65                70                75                80
Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val
                85                90                95
Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys
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Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala
115                120                125
Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met

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 165 170 175
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 Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala
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 Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly
 210 215 220
 Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val
 225 230 235 240
 Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe
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 Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu
 260 265 270
 Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His
 275 280 285
 Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg
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 <211> 483
 <212> DNA
 <213> Homo sapien

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 <211> 344
 <212> DNA
 <213> Homo sapien

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 <211> 592
 <212> DNA
 <213> Homo sapien

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104

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<210> 343

<211> 382

<212> DNA

<213> Homo sapien

<400> 343

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<210> 344

<211> 536

<212> DNA

<213> Homo sapien

<400> 344

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<210> 345

<211> 251

<212> DNA

<213> Homo sapien

<400> 345

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gcgtgggcca	ggaaatcaca	tcctacactg	cccaggagcc	agacacattt	atggaacaga	180
aaataacata	tcggatttgg	agagacactg	ccaactggct	ggagattaat	ccggacactg	240
gtgccatttc	c					251

<210> 346

<211> 282

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(282)

<223> n = A,T,C or G

<400> 346

cgcgtctctg	acactgtgat	catgacaggg	gttcaaacag	aaagtgcctg	ggccctcctt	60
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ctaagtcttg ttaccaaaaa aaggaaaaag aaaagatctt ctcagttaca aattctggga 120
aggagacta tacctggctc ttgccctaag tgagaggtct tccctccgc accaaaaaat 180
agaaaggctt tctatttcac tggcccaggt agggggaagg agagtaactt tgagtctgtg 240
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<210> 347

<211> 201

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(201)

<223> n = A,T,C or G

<400> 347

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acacacataa tattataaaa tgccatctaa ttggaaggag ctttctatca ttgcaagtca 60
taaataatac ttttaaaaa ntactancag cttttaccta ngctcctaaa tgcttgtaaa 120
tctgagactg actggaccca cccagaccca gggcaaagat acatgttacc atatcatctt 180
tataaagaat tttttttgt c 201

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<210> 348

<211> 251

<212> DNA

<213> Homo sapien

<400> 348

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ctgttaatca caacatttgt gcatcacttg tgccaagtga gaaaatgttc taaaatcaca 60
agagagaaca gtgccagaat gaaactgacc ctaagtccta ggtgccctg ggcaggcaga 120
aggagacact cccagcatgg aggagggtt atcttttcat cctaggtcag gtctacaatg 180
ggggaaggtt ttattataga actcccaaca gcccacctca ctctgcccac ccacccgatg 240
gccctgctc c 251

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<210> 349

<211> 251

<212> DNA

<213> Homo sapien

<400> 349

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taaaaaatcaa gccatttaat tgtatctttg aaggtaaaca atatatggga gctggatcac 60
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cagaagggtc tgaactctac gtgttaccag agaacataat gcaattcatg cattccactt 180
agcaattttg taaaatacca gaaacagacc ccaagagtct ttcaagatga ggaaaattca 240
actcctgggt t 251

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<210> 350

<211> 908

<212> DNA

<213> Homo sapien

<400> 350

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ctggacactt tgcgagggt tttgctggct gctgctgctg cccgtcatgc tactcatcgt 60
agcccgcccg gtgaagctcg ctgctttccc tacctcctta agtgactgcc aaacgccac 120
cggctggaat tgctctggtt atgatgacag agaaaaatgat ctcttcctct gtgacaccaa 180
cacctgtaaa tttgatggg aatgtttaag aattggagac actgtgactt gcgtctgtca 240
gttcaagtgc aacaatgact atgtgcctgt gtgtggctcc aatggggaga gctaccagaa 300
tgagtgttac ctgcgacagg ctgcatgcaa acagcagagt gagatacttg tgggtgcaga 360
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gtgtaatat gactgttctc aaaccaactt caatcccctc tgcgcttctg atgggaaatc 540
ttatgataat gcatgccaaa tcaaagaagc atcgtgtcag aaacaggaga aaattgaagt 600
catgtctttg ggtcgtatgc aagataacac aactacaact actaagtctg aagatgggca 660

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106

ttatgcaaga	acagattatg	cagagaatgc	taacaaatta	gaagaaagtg	ccagagaaca	720
ccacataoct	tgtccggaac	attacaatgg	cttctgcatg	catgggaagt	gtgagcattc	780
tatcaatatg	caggagccat	cttgcaagg	tgatgctgg	tatactggac	aacactgtga	840
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aatcgag						908

<210> 351
 <211> 472
 <212> DNA
 <213> Homo sapien

<400> 351						
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cattaact	attttaaaat	cagwtttgyg	agtcattttac	cacaagctaa	atgtgtacac	180
tatgataaaa	acaaccattg	tattcctgtt	tttctaaaca	gtcctaattt	ctaactactgt	240
atatacctt	cgacatcaat	gaactttgtt	ttcttttact	ccagtaataa	agtaggcaca	300
gatctgtcca	caacaaactt	gccctctcat	gccttgctc	tcaccatgct	ctgctccagg	360
tcagcccc	tttggcctgt	ttgttttgtc	aaaaacctaa	tctgcttctt	gcttttcttg	420
gtaatatata	tttaggggaag	atgttgcttt	gccacacac	gaagcaaagt	aa	472

<210> 352
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 352						
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caggctgcgt	tccgtcctta	cgatgaagac	cacgatgcag	tttccaaaca	ttgccactac	180
atacatggaa	aggaggggga	agccaaccca	gaaatgggct	ttctctaatac	ctgggataacc	240
aataagcaca	a					251

<210> 353
 <211> 436
 <212> DNA
 <213> Homo sapien

<400> 353						
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cacattatgg	tattattact	atactgatta	tatttatcat	gtgacttcta	attaraaaat	120
gtatccaaaa	gcaaacacagc	agatatata	aattaaagag	acagaagata	gacattaaca	180
gataaggcaa	cttatacatt	gacaatccaa	atccaataca	tttaaacatt	tgggaaatga	240
gggggacaaa	tggaaagccar	atcaaatttg	tgtaaaacta	ttcagtatgt	ttcccttgct	300
tcatgtctga	raaggctctc	ccttcaatgg	ggatgacaaa	ctccaaatgc	cacacaaatg	360
ttaacagaat	actagattca	cactggaacg	gggttaaaga	agaaattatt	ttctataaaa	420
gggctcctaa	tgtagt					436

<210> 354
 <211> 854
 <212> DNA
 <213> Homo sapien

<400> 354						
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atcaggggacc	accttttggg	ttgatatttt	gcttaatctg	catcttttga	gtaagatcat	180
ctggcagtag	aagctgttct	ccaggtacat	ttctctagct	catgtacaaa	aacatcctga	240
aggactttgt	caggtgcctt	gctaaaagcc	agatgcgttc	ggcacttctt	tggtctgagg	300
tttaattgcac	acctacaggc	actgggctca	tgctttcaag	tattttgtcc	tcactttagg	360
gtgagtga	gatccccatt	ataggagcac	ttgggagaga	tcatataaaa	gctgactctt	420
gagtacatgc	agtaatgggg	tagatgtgtg	tggtgtgtct	tcattcctgc	aagggtgctt	480

107

gttagggagt	gtttccagga	ggaacaagtc	tgaaccaat	catgaaataa	atggtaggtg	540
tgaactggaa	aactaattca	aaagagagat	cgatgatatca	gtgtggttga	tacaccttgg	600
caatatggaa	ggctctaatt	tgcccatatt	tgaataata	attcagcttt	ttgtaataca	660
aaataacaaa	ggattgagaa	tcatgggtgc	taatgtataa	aagaccagc	aaacataaat	720
atatcaactg	cataaatgta	aaatgcatgt	gacccaagaa	ggcccaaaag	tggcagacaa	780
cattgtaccc	attttccctt	ccaaaatgtg	agcggcgggc	ctgctgcttt	caaggctgtc	840
acacgggatg	tcag					854

<210> 355
 <211> 676
 <212> DNA
 <213> Homo sapien

<400> 355						
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atccacaagt	catacctgga	tgtcagcgaa	gagggcacgg	aggcagcagc	agccactggg	180
gacagcatcg	ctgtaaaaag	cctaccaatg	agagctcagt	tcaaggcgaa	ccacccttc	240
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gtgactttcc	cacggccaaa	aagctgttca	cacctcacgc	acctctgtgc	ctcagtttgc	420
tcactgtcaa	aataggtcta	ggatttcttc	caaccatttc	atgagttgtg	aagctaaggc	480
tttgttaatc	atggaaaaag	gtagacttat	gcagaaagcc	tttctggctt	tcttatctgt	540
gggtgtctcat	ttgagtgtcg	tccagtgtca	tgatcaagtc	aatgagtaaa	attttaaggg	600
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gcttaaagaa	aaccag					676

<210> 356
 <211> 574
 <212> DNA
 <213> Homo sapien

<400> 356						
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catgtggcac	ctgactggca	tcaaaccaaa	gttcgtaggc	caacaaagat	gggccactca	120
caagcttccc	attttagtat	ctcagtgcct	atgagtatct	gacacctgtt	cctctcttca	180
gtctcttagg	gaggcttaaa	tctgtctcag	gtgtgctaag	agtgccagcc	caaggkgttc	240
aaaagtccac	aaaactgcag	tctttgctgg	gatagtaagc	caagcagtcg	ctggacagca	300
gagttctttt	cttgggcaac	agataaccag	acaggactct	aatcgtgtct	ttattcaaca	360
ttcttctgtc	tctgcctaga	ctggaataaa	aagccaatct	ctctcgtggc	acaggaagg	420
agatacaagc	tcgtttacat	gtgatagatc	taacaaaggc	atctaccgaa	gtctgggtctg	480
gatagacggc	acagggagct	cttaggtcag	cgctgctggg	tggaggacat	tctgagtcc	540
agctttgcag	cctttgtgca	acagtacttt	ccca			574

<210> 357
 <211> 393
 <212> DNA
 <213> Homo sapien

<400> 357						
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taatatggkg	kcttggtcac	tatacttaaa	aatgcaccac	tcataaatat	ttaattcagc	120
aagccacaac	caaracttga	ttttatcaac	aaaaaccctt	aaatataaac	ggsaaaaaag	180
atagatataa	ttattccagt	ttttttaaaa	cttaaaarat	attccattgc	cgaattaara	240
araarataag	tgttatatgg	aaagaagggc	attcaagcac	actaaaraaa	cctgaggkaa	300
gcataatctg	tacaaaatta	aactgtcctt	tttggcattt	taacaaattt	gcaacgktct	360
tttttttctt	tttctgtttt	tttttttttt	tac			393

<210> 358
 <211> 630
 <212> DNA
 <213> Homo sapien

108

<400> 358

acagggtaaa	caggaggatc	cttgctctca	cggagcttac	attctagcag	gaggacaata	60
ttaatgttta	taggaaaatg	atgagtttat	gacaaaggaa	gtagatagtg	ttttacaaga	120
gcatagagta	gggaagctaa	tccagcacag	ggaggtcaca	gagacatccc	taaggaaagt	180
gagtttaaac	tgagagaagc	aagtgcctaa	actgaaggat	gtggtgaaga	agaagggaga	240
gtagaacaat	ttgggcagag	ggaaccttat	agaccctaag	gtgggaaggt	tcaaagaact	300
gaaagagagc	tagaacagct	ggagccgttc	tccggtgtaa	agaggagtca	aagagataag	360
attaaagatg	tgaagattaa	gatcttggtg	gcattcaggg	attggcactt	ctacaagaaa	420
tcactgaagg	gagtaatgtg	acattacttt	tcacttcagg	atggccattc	taactccagg	480
gggtagactg	gactaggtaa	gactggaggc	aggtagacct	cttctaaggc	ctgcgatagt	540
gaaagacaaa	aataagtggg	gaaattcagg	ggatagttaa	aatcagtagg	acttaatgag	600
caagccagag	gttcctccac	aacaaccagt				630

<210> 359

<211> 620

<212> DNA

<213> Homo sapien

<400> 359

acagcattcc	aaaatataca	tctagagact	aarrgtaaat	gctctatagt	gaagaagtaa	60
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ctcaccagaa	gaataaagt	ctctgccagt	tattaaagga	ttactgctgg	tgaattaaat	180
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aggattaaat	gttttaggaa	cagatatataa	gcttcgccac	ggaagagatg	gacaaagcac	300
aaagacaaca	tgatacctta	ggaagcaaca	ctacccttcc	aggcataaaa	tttgagagaaa	360
tgcaacatta	tgcttcatga	ataatatgta	gaaagaaggt	ctgatgaaaa	tgacatcctt	420
aatgtaagat	aactttataa	gaattctggg	tcaaataaaa	ttctttgaag	aaaacatcca	480
aatgtcattg	acttatcaaa	tactatcttg	gcatataacc	tatgaaggca	aaactaaaca	540
aacaaaaaagc	tcacaccaaa	caaaaccatc	aacttatttt	gtattctata	acatacgaga	600
ctgtaaagat	gtgacagtgt					620

<210> 360

<211> 431

<212> DNA

<213> Homo sapien

<400> 360

aaaaaaaaaa	agccagaaca	acatgtgata	gataatatga	ttggctgcac	acttcagac	60
tgatgaatga	tgaacgtgat	ggactattgt	atggagcaca	tcttcagcaa	gagggggaaa	120
tactcatcat	ttttggccag	cagttgtttg	atcaccaaac	atcatgccag	aatactcagc	180
aaaccttctt	agctcttgag	aagtcaaaat	ccgggggaat	ttattcctgg	caattttaat	240
tggaactcct	atgtgagagc	agcggctacc	cagctggggt	ggtggagcga	acccgtcact	300
agtgacatg	cagtggcaga	gtccttggtg	accacctaga	ggaatacaca	ggcacatgtg	360
tgatgccaa	cgtgacacct	gtagcactca	aatttgtctt	gtttttgtct	ttcgggtgtg	420
agattcttag	t					431

<210> 361

<211> 351

<212> DNA

<213> Homo sapien

<400> 361

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ttgggtcctc	tggtctcttg	ccaagtttcc	cagccactcg	agggagaaat	atcgggaggt	180
ttgacttctt	ccggggcttt	cccgagggtc	tcaccgtgag	ccctgcggcc	ctcagggtcg	240
caatcctgga	ttcaatgtct	gaaacctcgc	tctctgcctg	ctggacttct	gaggccgtca	300
ctgccactct	gtctctccagc	tctgacagct	cctcatctgt	ggtcctgttg	t	351

<210> 362

<211> 463

109

<212> DNA

<213> Homo sapien

<400> 362

acttcatcag gccataatgg gtgcctcccg tgagaatcca agcacctttg gactgcgcga	60
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ccccggtcac agaaatgacc aggttgggtg ttttcaggtg ccagtgcctg gtcagcagct	180
cgtaaaggat ttccgcgtcc gtgtcgcagg acagacgtat atacttcctt ttcttcccca	240
gtgtctcaaa ctgaatatcc ccaaaggcgt cggtaggaaa ttccttggtg tgtttcttgt	300
agttccattt ctcactttgg ttgatctggg tgccttccat gtgctggctc tgggcatagc	360
cacacttgca cacattctcc ctgataagca cgatgggtgt gacaggaagg aaggatttca	420
ttgagcctgc ttatggaaac tggatttgtt agcttaaata gac	463

<210> 363

<211> 653

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)..(653)

<223> n = A,T,C or G

<400> 363

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ctaacgaaac ttctcaccta tgagttgtaa agcagaaaata cctgnactac agacgagtgc	240
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<210> 364

<211> 401

<212> DNA

<213> Homo sapien

<400> 364

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acgtgcatag taaatcttta tatttgctat ggcgttgac tagaggactt ggactgcaac	360
aagtggatgc gcggaaaatg aaatcttctt caatagccca g	401

<210> 365

<211> 356

<212> DNA

<213> Homo sapien

<400> 365

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gactgtcacg atgtgtatag tacagtttga caagcctggg tccatacaga ccgctggaga	300
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110

<210> 366
 <211> 1851
 <212> DNA
 <213> Homo sapien

<400> 366
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 aagatacatc aacattttgc tcaagtagag ggctgactat acttgctgat ccacaacata 360
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 tgattaaaaa tttcaccact tgctgttttt gctcatgtat accaagtagc agtgggtgta 480
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 aatataattt tctctggag ccatatggat gaactatgaa ggaagaactc cccgaagaag 1440
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 cttttccca tttagtatta tgttggtgt gggctgtca taggtggtt ttattacttt 1800
 aaggtatgtc cttctatgc ctgttttgct gagggtttta attctcgtgc c 1851

<210> 367
 <211> 668
 <212> DNA
 <213> Homo sapien

<400> 367
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 gcagtcctat gagagtgaga agacttttta ggaattgtga gtgcactagc tacagccata 600
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 aaaaaaa 668

<210> 368
 <211> 1512
 <212> DNA
 <213> Homo sapien

<400> 368

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actccaagaa	aagttaaaca	tgtttcagtg	aatagagatc	ctgctccttt	ggcaagttcc	1440
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<210> 369

<211> 1853

<212> DNA

<213> Homo sapien

<400> 369

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ttcaaacaga	ttggaaaccc	ggagttacct	gctagttggt	gaaactggtt	ggtagacgcg	180
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tccatgcggg	ctgcttcttc	tgtgaagaag	ccatttggtc	tcaggagcaa	gatgggcaag	300
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112

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<210> 370

<211> 2184

<212> DNA

<213> Homo sapien

<400> 370

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tttcctctga	gaactgcaac	aataaataca	aggatgctgg	attttgtcaa	atgccttttc	180
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ttattgactt	gcctgtgtta	gaccggaaga	gctgggggtg	ttctcaggag	ccaccgtgtg	300
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ggagttcttc	cttcatagtt	catccatatg	gctccagagg	aaaattatat	tattttgtta	480
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<210> 371

<211> 1855

<212> DNA

<213> Homo sapien

<220>

<221> misc_feature

<222> (1)...(1855)

<223> n = A,T,C or G

<400> 371

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<210> 372

<211> 1059

<212> DNA

<213> Homo sapien

<400> 372

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<210> 373

<211> 1155

<212> DNA

<213> Homo sapien

<400> 373

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114

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<210> 374

<211> 2000

<212> DNA

<213> Homo sapien

<400> 374

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tcagaggaag	agtcacaaa	gcttgagggc	agtgaataatg	gccagccaga	gctagaaaat	1560
tttatggcta	tcgaagaaat	gaagaagcac	ggaagtactc	atgtcggatt	cccagaaaac	1620
ctgactaactg	gtgcactgc	tggaatgggt	gatgatggat	taattcctcc	aaggaagagc	1680
agaacacctg	aaagccagca	atttctctgac	actgagaatg	aagagtatca	cagtgacgaa	1740
caaaatgata	ctcagaagca	attttgtgaa	gaacagaaca	ctggaatatt	acacgatgag	1800
attctgattc	atgaagaaaa	gcagatagaa	gtggttgaaa	aatgaattc	tgagctttct	1860
cttagttgta	agaaagaaaa	agacatcttg	catgaaaaata	gtacgttgcg	ggaagaaatt	1920
gccatgctaa	gactggagct	agacacaatg	aaacatcaga	gccagctaaa	aaaaaaaaaa	1980
aaaaaaaaaa	aaaaaaaaaa					2000

<210> 375

115

<211> 2040
 <212> DNA
 <213> Homo sapien

<400> 375
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 aggagcaaga tgggcaagtg gtgctgccgt tgcctccctt gctgcaggga gagcggaag 120
 agcaacgtgg gcacttcttg agaccacgac gactctgcta tgaagacact caggagcaag 180
 atgggcaagt ggtgccgcca ctgcttcccc tgctgcaggg ggagtggcaa gagcaacgtg 240
 ggcgcttctg gagaccacga cgactctgct atgaagacac tcaggaacaa gatgggcaag 300
 tgggtgctgcc actgcttccc ctgctgcagg gggagcggca agagcaaggt gggcgcttg 360
 ggagactacg atgacagtgc cttcatggag ccaggtacc acgtccgtgg agaagatctg 420
 gacaagctcc acagagctgc ctgggtgggt aaagtcacca gaaaggatct catcgctatg 480
 ctcagggaca ctgacgtgaa caagaaggac aagcaaaaaga ggactgctct acatctggcc 540
 tctgccaatg ggaattcaga agtagtaaaa ctctgctgg acagacgatg tcaacttaat 600
 gtccttgaca acaaaaagag gacagctctg ataaaggccg tacaatgcca ggaagatgaa 660
 tgtgcgttaa tgttgctgga acatggcact gatccaaata ttccagatga gtatggaaat 720
 accactctgc actacgctat ctataatgaa gataaattaa tggccaaagc actgctctta 780
 tatggtgctg atatcgaatc aaaaaacaag catggcctca caccactgtt acttgggtga 840
 catgacgaaa aacagcaagt cgtgaaattt ttaatcaaga aaaaagcgaa tttaaatgca 900
 ctggatagat atggaaggac tgctctcata cttgctgtat gttgtggatc agcaagtata 960
 gtcagccttc tacttgagca aaatattgat gtatcttctc aagatctatc tggacagacg 1020
 gccagagagt atgctgttct tagtcatcat catgtaattt gccagttact ttctgactac 1080
 aaagaaaaac agatgctaaa aatctcttct gaaaacagca atccagaaca agacttaaa 1140
 ctgacatcag aggaagagtc acaaaaggct aaaggcagtg aaaatagcca gccagagaaa 1200
 atgtctcaag aaccagaaat aaataaggat ggtgatagag aggttgaaga agaaatgaag 1260
 aagcatgaaa gtaataatgt gggattacta gaaaacctga ctaatggtgt cactgctggc 1320
 aatggtgata atggattaat tcctcaaaag aagagcagaa cacctgaaaa tcagcaattt 1380
 cctgacaacg aaagtgaaga gtatcacaga atttgcgaat tagtttctga ctacaaagaa 1440
 aaacagatgc caaaatactc ttctgaaaac agcaaccag aacaagactt aaagctgaca 1500
 tcagaggaag agtcacaaag gcttgagggc agtgaaaatg gccagccaga gaaaagatct 1560
 caagaaccag aaataaataa ggatggtgat agagagctag aaaattttat ggctatcgaa 1620
 gaaatgaaga agcacggaag tactcatgtc ggattcccag aaaacctgac taatggtgac 1680
 actgctggca atggtgatga tggattaatt cctccaagga agagcagaac acctgaaagc 1740
 cagcaatttc ctgacactga gaatgaagag tatcacagt acgaacaaaa tgatactcag 1800
 aagcaatttt gtgaagaaca gaacactgga atattacacg atgagattct gattcatgaa 1860
 gaaaagcaga tagaagtgtg tgaaaaaatg aattctgagc tttctcttag ttgtaagaaa 1920
 gaaaaagaca tcttgcatga aaatagtacg ttgcgggaag aaattgccat gctaagactg 1980
 gagctagaca caatgaaaca tcagagccag ctaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040

<210> 376
 <211> 329
 <212> PRT
 <213> Homo sapien

<400> 376
 Met Asp Ile Val Val Ser Gly Ser His Pro Leu Trp Val Asp Ser Phe
 1 5 10 15
 Leu His Leu Ala Gly Ser Asp Leu Leu Ser Arg Ser Leu Met Ala Glu
 20 25 30
 Glu Tyr Thr Ile Val His Ala Ser Phe Ile Ser Cys Ile Ser Ser Ser
 35 40 45
 Leu Asp Gly Gln Gly Glu Arg Gln Glu Gln Arg Gly His Phe Trp Arg
 50 55 60
 Pro Gln Arg Leu Leu Cys Glu Asp Ala Trp Glu Gln Glu Val Gln Val
 65 70 75 80
 Val Leu Pro Leu Leu Pro Leu Leu Gln Gly Ser Gly Lys Ser Asn Val
 85 90 95
 Val Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe Met Asp Pro Arg Tyr
 100 105 110
 His Val His Gly Glu Asp Leu Asp Lys Leu His Arg Ala Ala Trp Trp
 115 120 125

116

Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met Leu Arg Asp Thr Asp
 130 135 140
 Val Asn Lys Arg Asp Lys Gln Lys Arg Thr Ala Leu His Leu Ala Ser
 145 150 155 160
 Ala Asn Gly Asn Ser Glu Val Val Lys Leu Val Leu Asp Arg Arg Cys
 165 170 175
 Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr Ala Leu Thr Lys Ala
 180 185 190
 Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met Leu Leu Glu His Gly
 195 200 205
 Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr
 210 215 220
 Ala Val Tyr Asn Glu Asp Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr
 225 230 235 240
 Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly Leu Thr Pro Leu Leu
 245 250 255
 Leu Gly Ile His Glu Gln Lys Gln Gln Val Val Lys Phe Leu Ile Lys
 260 265 270
 Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr Gly Arg Thr Ala Leu
 275 280 285
 Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile Val Ser Pro Leu Leu
 290 295 300
 Glu Gln Asn Val Asp Val Ser Ser Gln Asp Leu Glu Arg Arg Pro Glu
 305 310 315 320
 Ser Met Leu Phe Leu Val Ile Ile Met
 325

<210> 377
 <211> 148
 <212> PRT
 <213> Homo sapien

<220>
 <221> VARIANT
 <222> (1)...(148)
 <223> Xaa = Any Amino Acid

<400> 377
 Met Thr Xaa Pro Ser Trp Ser Pro Gly Thr Thr Ser Val Glu Lys Ile
 1 5 10 15
 Trp Thr Ser Ser Thr Glu Leu Pro Trp Trp Gly Lys Val Pro Arg Lys
 20 25 30
 Asp Leu Ile Val Met Leu Arg Asp Thr Asp Val Asn Lys Xaa Asp Lys
 35 40 45
 Gln Lys Arg Thr Ala Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu
 50 55 60
 Val Val Lys Leu Xaa Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp
 65 70 75 80
 Asn Lys Lys Arg Thr Ala Leu Xaa Lys Ala Val Gln Cys Gln Glu Asp
 85 90 95
 Glu Cys Ala Leu Met Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro
 100 105 110
 Asp Glu Tyr Gly Asn Thr Thr Leu His Tyr Ala Xaa Tyr Asn Glu Asp
 115 120 125
 Lys Leu Met Ala Lys Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser
 130 135 140
 Lys Asn Lys Val
 145

<210> 378
 <211> 1719
 <212> PRT

<213> Homo sapien

<400> 378

Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys
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Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe
			20					25					30		
Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp
		35					40					45			
His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp
	50					55					60				
Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val
	65				70					75					80
Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn
				85				90						95	
Lys	Met	Gly	Lys	Trp	Cys	Cys	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser
			100					105					110		
Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp	Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe
		115					120					125			
Met	Glu	Pro	Arg	Tyr	His	Val	Arg	Gly	Glu	Asp	Leu	Asp	Lys	Leu	His
	130					135					140				
Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val	Pro	Arg	Lys	Asp	Leu	Ile	Val	Met
	145				150					155					160
Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys	Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala
				165				170						175	
Leu	His	Leu	Ala	Ser	Ala	Asn	Gly	Asn	Ser	Glu	Val	Val	Lys	Leu	Leu
			180					185					190		
Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn	Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr
		195					200					205			
Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys	Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met
	210					215					220				
Leu	Leu	Glu	His	Gly	Thr	Asp	Pro	Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn
	225				230					235					240
Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr	Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys
				245				250						255	
Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp	Ile	Glu	Ser	Lys	Asn	Lys	His	Gly
			260					265					270		
Leu	Thr	Pro	Leu	Leu	Leu	Gly	Val	His	Glu	Gln	Lys	Gln	Gln	Val	Val
		275					280					285			
Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala	Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr
	290					295					300				
Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala	Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile
	305				310					315					320
Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn	Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu
				325				330						335	
Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr	Ala	Val	Ser	Ser	His	His	His	Val
				340				345					350		
Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr	Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile
		355					360					365			
Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu	Asn	Val	Ser	Arg	Thr	Arg	Asn	Lys
	370				375						380				
Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met	Pro	Ala	Ala	Ser
	385				390					395					400
Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys
				405				410						415	
Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys	Ser	Asn	Val	Gly
			420					425					430		
Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr	Leu	Arg	Ser	Lys
		435					440					445			
Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly
	450					455					460				
Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys

				965					970					975	
Cys	Glu	Glu	Gln	Asn	Thr	Gly	Ile	Leu	His	Asp	Glu	Ile	Leu	Ile	His
			980						985					990	
Glu	Glu	Lys	Gln	Ile	Glu	Val	Val	Glu	Lys	Met	Asn	Ser	Glu	Leu	Ser
		995					1000						1005		
Leu	Ser	Cys	Lys	Lys	Glu	Lys	Asp	Ile	Leu	His	Glu	Asn	Ser	Thr	Leu
	1010					1015					1020				
Arg	Glu	Glu	Ile	Ala	Met	Leu	Arg	Leu	Glu	Leu	Asp	Thr	Met	Lys	His
	1025				1030					1035					104
Gln	Ser	Gln	Leu	Pro	Arg	Thr	His	Met	Val	Val	Glu	Val	Asp	Ser	Met
			1045						1050					1055	
Pro	Ala	Ala	Ser	Ser	Val	Lys	Lys	Pro	Phe	Gly	Leu	Arg	Ser	Lys	Met
		1060							1065				1070		
Gly	Lys	Trp	Cys	Cys	Arg	Cys	Phe	Pro	Cys	Cys	Arg	Glu	Ser	Gly	Lys
		1075					1080					1085			
Ser	Asn	Val	Gly	Thr	Ser	Gly	Asp	His	Asp	Asp	Ser	Ala	Met	Lys	Thr
	1090					1095					1100				
Leu	Arg	Ser	Lys	Met	Gly	Lys	Trp	Cys	Arg	His	Cys	Phe	Pro	Cys	Cys
	1105				1110					1115					112
Arg	Gly	Ser	Gly	Lys	Ser	Asn	Val	Gly	Ala	Ser	Gly	Asp	His	Asp	Asp
			1125						1130					1135	
Ser	Ala	Met	Lys	Thr	Leu	Arg	Asn	Lys	Met	Gly	Lys	Trp	Cys	Cys	His
		1140							1145				1150		
Cys	Phe	Pro	Cys	Cys	Arg	Gly	Ser	Gly	Lys	Ser	Lys	Val	Gly	Ala	Trp
		1155					1160					1165			
Gly	Asp	Tyr	Asp	Asp	Ser	Ala	Phe	Met	Glu	Pro	Arg	Tyr	His	Val	Arg
	1170					1175					1180				
Gly	Glu	Asp	Leu	Asp	Lys	Leu	His	Arg	Ala	Ala	Trp	Trp	Gly	Lys	Val
	1185				1190					1195					120
Pro	Arg	Lys	Asp	Leu	Ile	Val	Met	Leu	Arg	Asp	Thr	Asp	Val	Asn	Lys
			1205						1210					1215	
Lys	Asp	Lys	Gln	Lys	Arg	Thr	Ala	Leu	His	Leu	Ala	Ser	Ala	Asn	Gly
		1220							1225				1230		
Asn	Ser	Glu	Val	Val	Lys	Leu	Leu	Leu	Asp	Arg	Arg	Cys	Gln	Leu	Asn
		1235					1240					1245			
Val	Leu	Asp	Asn	Lys	Lys	Arg	Thr	Ala	Leu	Ile	Lys	Ala	Val	Gln	Cys
		1250				1255					1260				
Gln	Glu	Asp	Glu	Cys	Ala	Leu	Met	Leu	Leu	Glu	His	Gly	Thr	Asp	Pro
	1265				1270					1275					128
Asn	Ile	Pro	Asp	Glu	Tyr	Gly	Asn	Thr	Thr	Leu	His	Tyr	Ala	Ile	Tyr
			1285						1290					1295	
Asn	Glu	Asp	Lys	Leu	Met	Ala	Lys	Ala	Leu	Leu	Leu	Tyr	Gly	Ala	Asp
		1300						1305					1310		
Ile	Glu	Ser	Lys	Asn	Lys	His	Gly	Leu	Thr	Pro	Leu	Leu	Gly	Val	
		1315					1320					1325			
His	Glu	Gln	Lys	Gln	Gln	Val	Val	Lys	Phe	Leu	Ile	Lys	Lys	Lys	Ala
		1330				1335					1340				
Asn	Leu	Asn	Ala	Leu	Asp	Arg	Tyr	Gly	Arg	Thr	Ala	Leu	Ile	Leu	Ala
	1345				1350					1355					136
Val	Cys	Cys	Gly	Ser	Ala	Ser	Ile	Val	Ser	Leu	Leu	Leu	Glu	Gln	Asn
			1365						1370				1375		
Ile	Asp	Val	Ser	Ser	Gln	Asp	Leu	Ser	Gly	Gln	Thr	Ala	Arg	Glu	Tyr
		1380						1385					1390		
Ala	Val	Ser	Ser	His	His	His	Val	Ile	Cys	Gln	Leu	Leu	Ser	Asp	Tyr
		1395					1400					1405			
Lys	Glu	Lys	Gln	Met	Leu	Lys	Ile	Ser	Ser	Glu	Asn	Ser	Asn	Pro	Glu
	1410					1415					1420				
Gln	Asp	Leu	Lys	Leu	Thr	Ser	Glu	Glu	Glu	Ser	Gln	Arg	Phe	Lys	Gly
	1425				1430					1435					144
Ser	Glu	Asn	Ser	Gln	Pro	Glu	Lys	Met	Ser	Gln	Glu	Pro	Glu	Ile	Asn
			1445						1450				1455		
Lys	Asp	Gly	Asp	Arg	Glu	Val	Glu	Glu	Glu	Met	Lys	Lys	His	Glu	Ser

120

1460 1465 1470
 Asn Asn Val Gly Leu Leu Glu Asn Leu Thr Asn Gly Val Thr Ala Gly
 1475 1480 1485
 Asn Gly Asp Asn Gly Leu Ile Pro Gln Arg Lys Ser Arg Thr Pro Glu
 1490 1495 1500
 Asn Gln Gln Phe Pro Asp Asn Glu Ser Glu Glu Tyr His Arg Ile Cys
 1505 1510 1515 152
 Glu Leu Val Ser Asp Tyr Lys Glu Lys Gln Met Pro Lys Tyr Ser Ser
 1525 1530 1535
 Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu Glu Glu
 1540 1545 1550
 Ser Gln Arg Leu Glu Gly Ser Glu Asn Gly Gln Pro Glu Lys Arg Ser
 1555 1560 1565
 Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Leu Glu Asn Phe
 1570 1575 1580
 Met Ala Ile Glu Glu Met Lys Lys His Gly Ser Thr His Val Gly Phe
 1585 1590 1595 160
 Pro Glu Asn Leu Thr Asn Gly Ala Thr Ala Gly Asn Gly Asp Asp Gly
 1605 1610 1615
 Leu Ile Pro Pro Arg Lys Ser Arg Thr Pro Glu Ser Gln Gln Phe Pro
 1620 1625 1630
 Asp Thr Glu Asn Glu Glu Tyr His Ser Asp Glu Gln Asn Asp Thr Gln
 1635 1640 1645
 Lys Gln Phe Cys Glu Glu Gln Asn Thr Gly Ile Leu His Asp Glu Ile
 1650 1655 1660
 Leu Ile His Glu Glu Lys Gln Ile Glu Val Val Glu Lys Met Asn Ser
 1665 1670 1675 168
 Glu Leu Ser Leu Ser Cys Lys Lys Glu Lys Asp Ile Leu His Glu Asn
 1685 1690 1695
 Ser Thr Leu Arg Glu Glu Ile Ala Met Leu Arg Leu Glu Leu Asp Thr
 1700 1705 1710
 Met Lys His Gln Ser Gln Leu
 1715

<210> 379
 <211> 656
 <212> PRT
 <213> Homo sapien

<400> 379
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175

Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu
 450 455 460
 Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu
 465 470 475 480
 Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp
 485 490 495
 Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu
 500 505 510
 Asn Gly Gln Pro Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys
 515 520 525
 Lys His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly
 530 535 540
 Ala Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser
 545 550 555 560
 Arg Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr
 565 570 575
 His Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln
 580 585 590
 Asn Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln
 595 600 605
 Ile Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys
 610 615 620
 Lys Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile
 625 630 635 640
 Ala Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu
 645 650 655

122

<211> 671
 <212> PRT
 <213> Homo sapien

<400> 380
 Met Val Val Glu Val Asp Ser Met Pro Ala Ala Ser Ser Val Lys Lys
 1 5 10 15
 Pro Phe Gly Leu Arg Ser Lys Met Gly Lys Trp Cys Cys Arg Cys Phe
 20 25 30
 Pro Cys Cys Arg Glu Ser Gly Lys Ser Asn Val Gly Thr Ser Gly Asp
 35 40 45
 His Asp Asp Ser Ala Met Lys Thr Leu Arg Ser Lys Met Gly Lys Trp
 50 55 60
 Cys Arg His Cys Phe Pro Cys Cys Arg Gly Ser Gly Lys Ser Asn Val
 65 70 75 80
 Gly Ala Ser Gly Asp His Asp Asp Ser Ala Met Lys Thr Leu Arg Asn
 85 90 95
 Lys Met Gly Lys Trp Cys Cys His Cys Phe Pro Cys Cys Arg Gly Ser
 100 105 110
 Gly Lys Ser Lys Val Gly Ala Trp Gly Asp Tyr Asp Asp Ser Ala Phe
 115 120 125
 Met Glu Pro Arg Tyr His Val Arg Gly Glu Asp Leu Asp Lys Leu His
 130 135 140
 Arg Ala Ala Trp Trp Gly Lys Val Pro Arg Lys Asp Leu Ile Val Met
 145 150 155 160
 Leu Arg Asp Thr Asp Val Asn Lys Lys Asp Lys Gln Lys Arg Thr Ala
 165 170 175
 Leu His Leu Ala Ser Ala Asn Gly Asn Ser Glu Val Val Lys Leu Leu
 180 185 190
 Leu Asp Arg Arg Cys Gln Leu Asn Val Leu Asp Asn Lys Lys Arg Thr
 195 200 205
 Ala Leu Ile Lys Ala Val Gln Cys Gln Glu Asp Glu Cys Ala Leu Met
 210 215 220
 Leu Leu Glu His Gly Thr Asp Pro Asn Ile Pro Asp Glu Tyr Gly Asn
 225 230 235 240
 Thr Thr Leu His Tyr Ala Ile Tyr Asn Glu Asp Lys Leu Met Ala Lys
 245 250 255
 Ala Leu Leu Leu Tyr Gly Ala Asp Ile Glu Ser Lys Asn Lys His Gly
 260 265 270
 Leu Thr Pro Leu Leu Leu Gly Val His Glu Gln Lys Gln Gln Val Val
 275 280 285
 Lys Phe Leu Ile Lys Lys Lys Ala Asn Leu Asn Ala Leu Asp Arg Tyr
 290 295 300
 Gly Arg Thr Ala Leu Ile Leu Ala Val Cys Cys Gly Ser Ala Ser Ile
 305 310 315 320
 Val Ser Leu Leu Leu Glu Gln Asn Ile Asp Val Ser Ser Gln Asp Leu
 325 330 335
 Ser Gly Gln Thr Ala Arg Glu Tyr Ala Val Ser Ser His His His Val
 340 345 350
 Ile Cys Gln Leu Leu Ser Asp Tyr Lys Glu Lys Gln Met Leu Lys Ile
 355 360 365
 Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp Leu Lys Leu Thr Ser Glu
 370 375 380
 Glu Glu Ser Gln Arg Phe Lys Gly Ser Glu Asn Ser Gln Pro Glu Lys
 385 390 395 400
 Met Ser Gln Glu Pro Glu Ile Asn Lys Asp Gly Asp Arg Glu Val Glu
 405 410 415
 Glu Glu Met Lys Lys His Glu Ser Asn Asn Val Gly Leu Leu Glu Asn
 420 425 430
 Leu Thr Asn Gly Val Thr Ala Gly Asn Gly Asp Asn Gly Leu Ile Pro
 435 440 445
 Gln Arg Lys Ser Arg Thr Pro Glu Asn Gln Gln Phe Pro Asp Asn Glu

123

450		455		460
Ser Glu Glu Tyr His Arg Ile Cys Glu Leu Val Ser Asp Tyr Lys Glu				
465		470		480
Lys Gln Met Pro Lys Tyr Ser Ser Glu Asn Ser Asn Pro Glu Gln Asp				
	485		490	495
Leu Lys Leu Thr Ser Glu Glu Glu Ser Gln Arg Leu Glu Gly Ser Glu				
	500		505	510
Asn Gly Gln Pro Glu Lys Arg Ser Gln Glu Pro Glu Ile Asn Lys Asp				
	515		520	525
Gly Asp Arg Glu Leu Glu Asn Phe Met Ala Ile Glu Glu Met Lys Lys				
	530		535	540
His Gly Ser Thr His Val Gly Phe Pro Glu Asn Leu Thr Asn Gly Ala				
545		550		560
Thr Ala Gly Asn Gly Asp Asp Gly Leu Ile Pro Pro Arg Lys Ser Arg				
	565		570	575
Thr Pro Glu Ser Gln Gln Phe Pro Asp Thr Glu Asn Glu Glu Tyr His				
	580		585	590
Ser Asp Glu Gln Asn Asp Thr Gln Lys Gln Phe Cys Glu Glu Gln Asn				
	595		600	605
Thr Gly Ile Leu His Asp Glu Ile Leu Ile His Glu Glu Lys Gln Ile				
	610		615	620
Glu Val Val Glu Lys Met Asn Ser Glu Leu Ser Leu Ser Cys Lys Lys				
625		630		640
Glu Lys Asp Ile Leu His Glu Asn Ser Thr Leu Arg Glu Glu Ile Ala				
	645		650	655
Met Leu Arg Leu Glu Leu Asp Thr Met Lys His Gln Ser Gln Leu				
	660		665	670

<210> 381
 <211> 251
 <212> DNA
 <213> Homo sapien

<400> 381
 ggagaagcgt ctgctggggc aggaaggggt ttccctgccc tctcacctgt ccctcaccaa 60
 ggtaacatgc ttcccctaag ggtatcccaa cccaggggcc tcaccatgac ctctgagggg 120
 ccaatatccc aggagaagca ttggggaggt gggggcaggt gaaggacca ggactcacac 180
 atcctggggc tccaaggcag aggagagggt cctcaagaag gtcaggagga aaatccgtaa 240
 caagcagtca g 251

<210> 382
 <211> 3279
 <212> DNA
 <213> Homo sapiens

<400> 382
 cttcctgcag ccccatgct ggtgaggggc acgggcagga acagtggacc caacatggaa 60
 atgctggagg gtgtcaggaa gtgatcgggc tctggggcag ggaggagggg tggggagtgt 120
 cactgggagg ggacatcctg cagaaggtag gactgagcaa acaccgctg caggggaggg 180
 gagagccctg cggcacctgg gggagcagag ggagcagcac ctgcccaggc ctgggaggag 240
 gggcctggag ggcgtgagga ggagcaggg ggctgcatgg ctggagttag ggatcagggg 300
 cagggcgcga gatggcctca cacagggaag agagggcccc tcctgcaggg cctcacctgg 360
 gccacaggag gacactgctt ttcctctgag gactcaggag ctgtggatgg tgctggacag 420
 aagaaggaca gggcctggct cagggtcca gaggtgtcg ctggcttccc tttgggatca 480
 gactgcaggg agggaggcgg gcagggtgtg ggggggagtg acgatgagga tgacctgggg 540
 gtggctccag gccttgcccc tgctggggc ctcaccagc ctccctcaca gtctcctggc 600
 cctcagtcct tcccctccac tccatcctcc atctggcctc agtgggtcat tctgatcact 660
 gaactgacca taccagccc tgcccacggc cctccatggc tccccaatgc cctggagagg 720
 ggacatctag tcagagagta gtcctgaaga ggtggcctct gcgatgtgcc tgtgggggca 780
 gcatcctgca gatggtccc gcccctcatcc tgctgacctg tctgcaggga ctgtcctcct 840
 ggaccttgcc ccttggtgag gagctggacc ctgaagtccc ctccccatag gccaaactg 900
 gagccttggt ccctctgttg gactccctgc ccatattctt gtgggagtgg gttctggaga 960

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catttctgtc tgttcctgag agctgggaat tgctctcagt catctgcctg cgcggttctg 1020
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atcatggggc cctgagccat gtgccctgcc tgaaaagcct gctgtgtaca ccaagggtgt 1200
gcattaccgg aagtggatca aggacaccat cgcagccaac ccctgagtgc ccctgtccca 1260
cccctacctc tagtaaattt aagtccacct cacgttcttg catcacttgg cctttctgga 1320
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gacctgtgct ttctggtgtg gagtccaggg ctgctaggaa aaggaatggg cagacacagg 1440
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ctctgaagac ttctcgtca gtttcagtga ggacacacac aaagacgtgg gtgacctgt 1560
tgtttgtggg gtgcagagat gggaggggtg gggcccaccc tggagagtg gacagtgaca 1620
caaggtggac actctctaca gatcactgag gataagctgg agccacaatg catgaggcac 1680
acacacagca aggttgacgc tgtaaacata gcccacgctg tcctggggggc actgggaagc 1740
ctagataagg ccgtgagcag aaagaagggg aggatcctcc tatgttgttg aaggagggac 1800
tagggggaga aactgaaagc tgattaatta caggagggtt gtccaggctc ccaaaccac 1860
cgtcagattt gatgatttcc tagcaggact tacagaaata aagagctatc atgctgtggt 1920
ttattatggt ttgttacatt gataggatac atactgaaat cagcaaacaa aacagatgta 1980
tagattagag tgtggagaaa acagaggaaa acttgcagtt acgaagactg gcaacttggc 2040
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gtagctgac cagctgatag aggaactagc cagggtgggg cctttccctt tggatggggg 2160
gcatatccga cagttattct ctccaagtgg agacttacgg acagcatata attctccctg 2220
caaggatgta tgataatatg taaaagtaa ttccaactga ggaagctcac ctgacctta 2280
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cagatgtaca aaaacaggga ttcatcacia atcccatctt tagcatgaag ggtctggcat 2460
ggcccaaggc cccaagtata tcaaggcact tgggcagaac atgccaagga atcaaagtgc 2520
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aaagaagaat ccagaaatag gggcacattg aggaatgata ctgagcccaa agagcattca 2760
atcattgttt tatttgcctt cttttcacac cattggtgag ggagggatta ccaccctggg 2820
gttatgaaga tggttgaaca cccacacat agcaccggag atatgagatc aacagtttct 2880
tagccataga gattcacagc ccagagcagg aggacgctgc acaccatgca ggatgacatg 2940
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gttttgagac tggcaggtag tgaaactcat taggctgaga acctgtgga atgcagctga 3120
cccagctgat agaggaaagta gccaggtggg agcctttccc agtgggtgtg ggacatatct 3180
ggcaagattt tgtggcactc ctggttacag atactggggc agcaaataaa actgaatctt 3240
gttttcagac cttaaaaaaa aaaaaaaaaa aaaagtttt 3279

```

<210> 383

<211> 155

<212> PRT

<213> Homo sapiens

<400> 383

Met Ala Gly Val Arg Asp Glu Gly Gln Gly Ala Arg Trp Pro His Thr
5 10 15

Gly Lys Arg Gly Pro Leu Leu Gln Gly Leu Thr Trp Ala Thr Gly Gly
20 25 30

His Cys Phe Ser Ser Glu Glu Ser Gly Ala Val Asp Gly Ala Gly Gln
35 40 45

Lys Lys Asp Arg Ala Trp Leu Arg Cys Pro Glu Ala Val Ala Gly Phe
50 55 60

Pro Leu Gly Ser Asp Cys Arg Glu Gly Gly Arg Gln Gly Cys Gly Gly
65 70 75 80

Ser Asp Asp Glu Asp Asp Leu Gly Val Ala Pro Gly Leu Ala Pro Ala

125

	85		90		95										
Trp	Ala	Leu	Thr	Gln	Pro	Pro	Ser	Gln	Ser	Pro	Gly	Pro	Gln	Ser	Leu
			100					105					110		
Pro	Ser	Thr	Pro	Ser	Ser	Ile	Trp	Pro	Gln	Trp	Val	Ile	Leu	Ile	Thr
		115					120					125			
Glu	Leu	Thr	Ile	Pro	Ser	Pro	Ala	His	Gly	Pro	Pro	Trp	Leu	Pro	Asn
	130					135					140				
Ala	Leu	Glu	Arg	Gly	His	Leu	Val	Arg	Glu						
145						150									

<210> 384
 <211> 557
 <212> DNA
 <213> Homo sapiens

<400> 384
 ggatcctcta gaggcgccgc ctactactac taaattcgcg gccgcgtcga cgaagaagag 60
 aaagatgtgt tttgttttgg actctctgtg gtcccttcca atgctgtggg tttccaacca 120
 ggggaagggt cctttttgca ttgccaagtg ccataaccat gaggactact ctaccatggg 180
 tctgcctcct ggccaagcag gctggtttgc aagaatgaaa tgaatgattc tacagctagg 240
 acttaacctt gaaatggaaa gtcttgcaat cccatttgca ggatccgtct gtgcacatgc 300
 ctctgtagag agcagcattc ccagggacct tggaaacagt tggcactgta aggtgcttgc 360
 tccccagac acatcctaaa aggtgttgta atggtgaaaa cgtcttcctt ctttattgcc 420
 ccttcttatt tatgtgaaca actgtttgtc tttttttgta tcttttttaa actgtaaaag 480
 tcaattgtga aaatgaatat catgcaaata aattatgcga ttttttttcc aaagtaaaaa 540
 aaaaaaaaaa aaaaaaa 557

<210> 385
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 385
 ttcccagggt atgtgcgagg gaagacacat ttactatcct tgatggggct gattccttta 60
 gtttctctag cagcagatgg gttaggagga agtgacccaa gtggttgact cctatgtgca 120
 tctcaaagcc atctgctgtc ttogagtacg gacacatcat cactcctgca ttgttgatca 180
 aaacgtggag gtgcttttcc tcagctaaga agcccttagc aaaagctcga atagacttag 240
 tatcagacag gtccagtttc cgcaccaaca cctgctggtt ccctgtcgtg gtctggatct 300
 ctttggccac caattcccc ttttccacat cccggca 337

<210> 386
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 386
 gggcccgcta ccggcccgag ccccgccctc cgagtcctcc tccccgggtg cctgcccgca 60
 gccgcgtcgg ccagaggggt gggcgcgggg ctgcctctac cggttgccgg ctgtaactca 120
 gcgaccttgg ccggaaggct ctagcaagga cccaccgacc ccagccgcgg cggcgggcgc 180
 gcggactttg cccggtgtgt gggcgggagc ggactgcgtg tccgcgagc ggcagcgaag 240
 atgttagcct tcgctgccag gaccgtggac cgatcccgag gctgtggtgt aacctcagcc 300

<210> 387
 <211> 537
 <212> DNA
 <213> Homo sapiens

126

<400> 387

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gggccgagtc gggcaccaag ggactctttg caggcttcct tcctcggatc atcaaggctg 60
ccccctcctg tgccatcatg atcagcacct atgagttcgg caaaagcttc ttccagaggc 120
tgaaccagga ccggcttctg ggcggtgaa aggggcaagg aggcaaggac cccgtctctc 180
ccacggatgg ggagagggca ggaggagacc cagccaagtg ccttttcctc agcactgagg 240
gagggggctt gtttcccttc cctcccggcg acaagctcca gggcagggct gtccctctgg 300
gcggcccagc acttcctcag acacaacttc ttcctgctgc tccagtcgtg gggatcatca 360
cttaccacc ccccaagttc aagaccaa atctccagctg ccccttcgt gtttccctgt 420
gtttgctgta gctgggcatg tctccaggaa ccaagaagcc ctgagcctgg tgtagtctcc 480
ctgacccttg ttaattcctt aagtctaaag atgatgaact tcaaaaaaaa aaaaaaa 537

```

<210> 388

<211> 520

<212> DNA

<213> Homo sapiens

<400> 388

```

aggataattt ttaaaccaat caaatgaaaa aaacaaacaa acaaaaaagg aaatgtcatg 60
tgaggttaaa ccagtttgca ttccccta atgtgaaaaa taagaggact actcagcact 120
gtttgaagat gttctcttct acagcttctg agaattgtgt tatttcactt gccaaagtga 180
ggacccccct cccaacatgc cccagcccac ccctaagcat ggtcccttgt caccaggcaa 240
ccaggaaact gctacttgtg gacctacca gagaccagga gggtttggtt agctcacagg 300
acttccccca cccagaaga ttagcatccc atactagact catactcaac tcaactaggc 360
tcatactcaa ttgatgggta ttagacaatt ccatttcttt ctgggtatta taaacagaaa 420
atctttcctc ttctcattac cagtaaaggc tcttggtatc tttctgttgg aatgatttct 480
atgaacttgt cttattttta tgggtgggtt tttttctggt 520

```

<210> 389

<211> 365

<212> DNA

<213> Homo sapiens

<400> 389

```

cgttgcccc gtttgacaga aggaaaggcg gagcttattc aaagtctaga gggagtggag 60
gagtttaaggc tggatttcag atctgcctgg ttccagccgc agtggtgccct ctgctcccc 120
aacgactttc caaataatct caccagcgcc ttccagctca ggcgtcctag aagcgtcttg 180
aagcctatgg ccagctgtct ttgtgttccc tctcaccgcg ctgtcctcac agctgagact 240
cccaggaaac cttcagacta ccttcctctg ccttcagcaa ggggcgttgc ccacattctc 300
tgagggtcag tggagaagcc tagactccca ttgctagagg tagaaagggg aagggtgctg 360
gggag

```

<210> 390

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(221)

<223> n = A,T,C or G

<400> 390

```

tgctctcca tcctggcccc gaattctctg tcaggaaagt ggggatggac cccatctgca 60
tacacgntt ctcattgggtg tggaacatct ctgcttgcgg ttccaggaag gcctctggct 120
gctctangag tctgancnga ntcgttgccc cantntgaca naaggaaagg cggagcttat 180
tcaaagtcta gagggagtgg aggagttaag gctggatttc a

```

<210> 391

<211> 325

<212> DNA

<213> Homo sapiens

127

<220>
 <221> misc_feature
 <222> (1)...(325)
 <223> n = A,T,C or G

<400> 391
 tggagcaggt cccgaggcct ccctagagcc tggggccgac tctgtgncga tgcangcttt 60
 ctctcgcgcc cagcctggag ctgctcctgg catctacca caatcagncg aggcgagcag 120
 tagccagggc actgctgcc aacagccagtc cnnataccat catgtnaccc ggtgngctct 180
 naanttn gat ntccanagcc ctaccatcn tagttctgct ctcccaccgg ntaccagccc 240
 cactgccag gaatcctaca gccagtaccc tgtcccgcag tctctaccta ccagtacgat 300
 gagacctccg gctactacta tgacc 325

<210> 392
 <211> 277
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(277)
 <223> n = A,T,C or G

<400> 392
 atattgttta actccttcct ttatatcttt taacattttc atggngaaa gttcacatct 60
 agtctcactt nggcnagn gn ctectacttg agtctcttcc cgggcctggn ccagtnagna 120
 antaccanga accgncatgn cttanaa ncttggtttn tgggttnntc aatgactgca 180
 tgcagtgcac caccctgtcc actacgtgat gctgtaggat taaagtctca cagtgggcgg 240
 ctgaggatag agcgccgcgt cctgtgttgc tggggaa 277

<210> 393
 <211> 566
 <212> DNA
 <213> Homo sapiens

<400> 393
 actagtcag tgtggtggaa ttgcgcccgc cgtcgacgga caggtcagct gtctggctca 60
 gtgatctaca ttctgaagtt gtctgaaaat gtcttcatga ttaaattcag cctaaacgtt 120
 ttgcccggaa cactgcagag acaatgctgt gagtttccaa ccttagccca tctgcgggca 180
 gagaaggtct agtttgtcca tcagcattat catgatata ggactgggta cttgggttaag 240
 gaggggtcta ggagatctgt cctttttaga gacaccttac ttataatgaa gtatttggga 300
 ggggtgtttt caaaagtaga aatgtcctgt attccgatga tcatcctgta aacattttat 360
 catttattaa tcatccctgc ctgtgtctat tattatattc atatctctac gctggaaact 420
 ttctgcctca atgtttactg tgcctttgtt tttgctagtt tgtgttgttg aaaaaaaaaa 480
 cattctctgc ctgagtttta atttttgtcc aaagttattt taatctatac aattaaaagc 540
 ttttgcctat caaaaaaaaaa aaaaaa 566

<210> 394
 <211> 384
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(384)
 <223> n = A,T,C or G

<400> 394
 gaacatacat gtcccggcac ctgagctgca gtctgacatc atcgccatca cgggcctcgc 60
 tgcaaattn gaccggggca aggctggact gctggagcgt gtgaaggagc tacaggccna 120
 gcaggaggac cgggctttta ggagttttta gctgagtgct actgtagacc ccaaatacca 180
 tcccaagatt atcgggagaa agggggcagc aattacccaa atccggttg agcatgacgt 240

128

```

gaacatccag tttcctgata aggacgatgg gaaccagccc caggaccaa ttaccatcac 300
agggtacgaa aagaacacag aagctgccag ggatgctata ctgagaattg tgggtgaact 360
tgagcagatg gtttctgagg acgt 384

```

```

<210> 395
<211> 399
<212> DNA
<213> Homo sapiens

```

```

<400> 395
ggcaaaactg tgtgacctca ataagacctc gcagatccaa ggtcaagtat cagaagtgc 60
tctgaccttg gactccaaga cctacatcaa cagcctggct atattagatg atgagccagt 120
tatcagaggt ttcattcattg cggaaattgt ggagtctaag gaaatcatgg cctctgaagt 180
attcacgtct ttccagtacc ctgagttctc tatagagttg cctaacacag gcagaattgg 240
ccagctactt gtctgcaatt gtatcttcaa gaataccctg gccatccctt tgactgacgt 300
caagttctct ttggaaagcc tgggcatctc ctactacag acctctgacc atgggacggt 360
gcagcctggt gagaccatcc aatcccaaata aaaatgcac 399

```

```

<210> 396
<211> 403
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(403)
<223> n = A,T,C or G

```

```

<400> 396
tggagttntc agtgcaaaaca agccataaaag cttcagtagc aaattactgt ctcacagaaa 60
gacattttca acttctgctc cagctgctga taaaacaaat catgtgttta gcttgactcc 120
agacaaggac aacctgttcc ttcataactc tctagagaaa aaaaggagtt gttagtagat 180
actaaaaaaa gtggatgaat aatctggata tttttcctaa aaagattcct tgaaacacat 240
taggaaaatg gagggcctta tgatcagaat gctagaatta gtccattgtg ctgaagcagg 300
gtttagggga gggagtgagg gataaaaagaa ggaaaaaaag aagagtgaga aaacctat 360
atcaaagcag gtgctatcac tcaatgttag gccctgctct ttt 403

```

```

<210> 397
<211> 100
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(100)
<223> n = A,T,C or G

```

```

<400> 397
actagtnacg tgtggtggaa ttcgcggccg cgtcgaccta naanccatct ctatagcaaa 60
tccatccccg ctctggttg gtnacagaat gactgacaaa 100

```

```

<210> 398
<211> 278
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(278)
<223> n = A,T,C or G

```

```

<400> 398

```

129

```

gcggccgcgt cgacagcagt tccgccagcg ctgcgccctg ggtgggggatg tgctgcacgc 60
ccacctggac atctggaagt cagcggcctg gatgaaagag cggacttcac ctggggcgat 120
tcactactgt gcctcgacca gtgaggagag ctggaccgac agcgagggtg actcatcatg 180
ctccgggcag cccatccacc tgtggcagtt cctcaaggag ttgctactca agccccacag 240
ctatggccgc ttcattangt ggctcaacaa ggagaagg 278

```

```

<210> 399
<211> 298
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(298)
<223> n = A,T,C or G

```

```

<400> 399
acggagggtg aggaagcgnc cctgggatcg anaggatggg tcctgncatt gaccncctcn 60
ggggtgccng catggagcgc atgggcgcgg gcctggggcca cgcatggat cgctggggct 120
ccgagatcga gcgcatgggc ctggatcatgg accgcatggg ctccgtggag cgcatgggct 180
ccggcattga gcgcatgggc ccgctggggc tcgaccacat ggctccanc attgancgca 240
tgggccagac catggagcgc attggctctg gcgtggagcn catgggtgcc ggcatggg 298

```

```

<210> 400
<211> 548
<212> DNA
<213> Homo sapiens

```

```

<400> 400
acatcaacta cttcctcatt ttaaggatg gcagttccct tcatcccctt ttctgcctt 60
gtacatgtac atgtatgaaa tttccttctc ttaccgaact ctctccacac atcacaaggt 120
caaagaacca cagccttaga agggtaagag ggcaccctat gaaatgaaat ggtgatttct 180
tgagtctctt ttttccacgt ttaagggggc atggcaggac ttagagttgc gagttaagac 240
tgcagagggc tagagaatta tttcatacag gctttgaggc caccatgtc acttatccc 300
tataacctct caccatcccc ttgtctactc tgatgcccc aagatgcaac tgggcagcta 360
gttgccccca taattctggg cctttgttgt ttgttttaat tacttgggca tcccaggaag 420
ctttccagtg atctcctacc atgggcccc ctccctggg atcaagcccctc ccaggccctg 480
tccccagccc ctctgcccc agcccacccg cttgccttgg tgctcagccc tcccattggg 540
agcaggtt 548

```

```

<210> 401
<211> 355
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(355)
<223> n = A,T,C or G

```

```

<400> 401
actgtttcca tggtatgttt ctacacattg ctacctcagt gctcctggaa acttagcttt 60
tgatgtctcc aagtagtcca ccttcattta actctttgaa actgtatcat ctttgccaag 120
taagagtggg ggcctatttc agctgctttg acaaaatgac tggctcctga cttaacgttc 180
tataaatgaa tgtgctgaag caaagtggcc atgggtggcg cgaagaagan aaagatgtgt 240
tttgttttgg actctctgtg gtcccttcca atgctgnngg tttccaacca ggggaagggt 300
cccttttgca ttgccaagtg ccataaccat gagcactact ctaccatggn tctgc 355

```

```

<210> 402
<211> 407
<212> DNA
<213> Homo sapiens

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130

<220>
 <221> misc_feature
 <222> (1)...(407)
 <223> n = A,T,C or G

<400> 402
 atggggcaag ctggataaag aaccaagacc cactggagta tgctgtcttc aagaaaccca 60
 tctcacatgc ggtggcatal ataggctcaa aataaaggaa tggagaaaaa tatttcaagc 120
 aaatggaaaa cagaaaaaag cagggtgttg actcctactt tctgacaaaa cagactatgc 180
 gaataaagat aaaaaagaga aggacattac aaagggtggtc ctgacctttg ataaatctca 240
 ttgcttgata ccaacctggg ctgttttaat tgccaaaacc aaaaggataa tttgctgagg 300
 ttgtggagct tctcccctgc agagagtccc tgatctccca aaatttggtt gagatgtaag 360
 gntgattttg ctgacaactc cttttctgaa gttttactca tttccaa 407

<210> 403
 <211> 303
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(303)
 <223> n = A,T,C or G

<400> 403
 cagtatttat agccnaactg aaaagctagt agcaggcaag tctcaaatcc aggcacccaa 60
 tcctaagcaa gagccatggc atggtgaaaa tgcaaaagga gagtctggcc aatctacaaa 120
 tagagaacaa gacctactca gtcattgaaca aaaaggcaga caccaacatg gatctcatgg 180
 gggattggat attgtaatta tagagcagga agatgacagt gatcgtcatt tggcacaaca 240
 tcttaacaac gaccgaaacc cattattttac ataaacctcc attcggtaac catgttgaaa 300
 gga 303

<210> 404
 <211> 225
 <212> DNA
 <213> Homo sapiens

<400> 404
 aagtgttaact tttaaaaatt tagtggattt tgaaaattct tagaggaaag taaaggaaaa 60
 attgttaatg cactcattta cctttacatg gtgaaagtgc tctcttgatc ctacaaacag 120
 acattttcca ctcggtgttc catagtgtgt aagtgtatca gatgtgttgg gcatgtgaat 180
 ctccaagtgc ctgtgtaata aataaagtat ctttatttca ttcatt 225

<210> 405
 <211> 334
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(334)
 <223> n = A,T,C or G

<400> 405
 gagctgttat actgtgagtt ctactaggaa atcatcaa atcgtagggtt tctggaggac 60
 ttcaatacac ctccccccat agtgaatcag cttccagggt gtccagtccc tctccttact 120
 tcatccccat cccatgccaa aggaagaccc tccctccttg gctcacagcc ttctctaggc 180
 ttcccagtgct ctccaggaca gagtgggtta tgttttcagc tccatccttg ctgtgagtg 240
 ctggtgcggt tgtgcctcca gttctgtctc agtgcttcac ggacagtgtc cagcccatgt 300
 cactctccac tctctcanng tggatccac ccct 334

131

<210> 406
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(216)
 <223> n = A,T,C or G

<400> 406
 ttccatcacct aatgagggag ttganatnac atnnaaccag gaaatgcatg gatctcaang 60
 gaaacaaaca cccaataaac tcggagtggc agactgacaa ctgtgagaca tgcacttgct 120
 acnaaacaca aatttnatgt tgcacccttg tttctacacc tgtgggttat gacaaagaca 180
 actgccaaaag aatnttcaag aaggaggact gccant 216

<210> 407
 <211> 413
 <212> DNA
 <213> Homo sapiens

<400> 407
 gctgacttgc tagtâtcatc tgcattcatt gaagcacaag aacttcacgc cttgactcat 60
 gtaaatgcaa taggattaaa aaataaattt gatatcacat ggaaacagac aaaaaatatt 120
 gtacaacatt gcacccagtgc tcagattcta cacctggcca ctgaggaagc aagagttaat 180
 cccagaggtc tatgtcctaa tgtgttatgg caaatggatg tcatgcacgt accttcattt 240
 ggaaaattgt catttgtcca tgtgacagtt gatacttatt cacatttcac atgggcaacc 300
 tgccagacag gagaaagtct tcccatgtta aaagacattt attatcttgt tttcctgtca 360
 tgggagttcc agaaaaagtt aaaacagaca atggggcagg ttctgtagta aag 413

<210> 408
 <211> 183
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(183)
 <223> n = A,T,C or G

<400> 408
 ggagctngcc ctcaattcct ccatntctat gttancatat ttaatgtctt ttgnnattaa 60
 tnccttaacta gttaatcctt aaagggtan ntaatcctta actagtcctt ccattgtgag 120
 cattatcctt ccagtattcn ccttctnttt tatttactcc ttcttggtta cccatgtact 180
 ntt 183

<210> 409
 <211> 250
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(250)
 <223> n = A,T,C or G

<400> 409
 cccacgcatg ataagctctt tatttctgta agtcctgcta ggaaatcatc aaatctgacg 60
 gtggtttggg ggacctgaac aaacctcctg taattaatca gctttcagtt tctcccccta 120
 gtccctcctt caacaacata ggaggatcct ccccttcttt ctgctcacgg ccttatctag 180
 gcttcccagt gccccagga cagcgtgggc tatgtttaca gcgcntcctt gctggggggg 240
 ggccntatgc 250

132

<210> 410
 <211> 306
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(306)
 <223> n = A,T,C or G

<400> 410
 ggctggtttg caagaatgaa atgaatgatt ctacagctag gacttaacct tgaaatggaa 60
 agtcttgcaa tcccatttgc aggatccgtc tgtgcacatg cctctgtaga gagcagcatt 120
 cccagggaacc ttggaaacag ttggcactgt aagggtgctt ctocccaaga cacatcctaa 180
 aagggtgtgt aatggtgaaa accgcttcct tctttattgc cccttcttat ttatgtgaac 240
 nactggttgg ctttttttgn atctttttta aactggaaag ttcaattgng aaaatgaata 300
 tcntgc 306

<210> 411
 <211> 261
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(261)
 <223> n = A,T,C or G

<400> 411
 agagatattn cttaggtnaa agttcataga gttcccatga actatatgac tggccacaca 60
 ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
 tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
 aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
 cttctctcaa gngagggcaa a 261

<210> 412
 <211> 241
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(241)
 <223> n = A,T,C or G

<400> 412
 gttcaatggt acctgacatt tctacaacac ccactcacc gatgtattcg ttgccagtg 60
 ggaacatacc agcctgaatt tggaaaaaat aattgtgttt cttgccagg aaatactacg 120
 actgactttg atggctccac aaacataacc cagtgtaaaa acagaagatg tggaggggag 180
 ctgggagatt tcaactgggta cattgaattc ccaaactacc cangcaatta cccagccaac 240
 a 241

<210> 413
 <211> 231
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(231)
 <223> n = A,T,C or G

133

<400> 413
aactcttaca atccaagtga ctcatctgtg tgcttgaatc ctttccactg tctcatctcc 60
ctcatccaag ttcttagtac ctctcttttg ttgtgaagga taatcaaact gaacaacaaa 120
aagttttact tcttcatttg gaacctaaaa actctcttct tcttgggtct gagggctcca 180
agaatccttg aatcanttct cagatcattg gggacaccan atcaggaacc t 231

<210> 414
<211> 234
<212> DNA
<213> Homo sapiens

<400> 414
actgtccatg aagcactgag cagaagctgg aggcacaacg caccagacac tcacagcaag 60
gatggagctg aaaacataac ccactctgtc ctggaggcac tgggaagcct agagaaggct 120
gtgagccaag gagggagggt cttccttttg catgggatgg ggatgaagta aggagaggga 180
ctggaccccc tggaagctga ttcactatgg ggggagggtg attgaagtcc tcca 234

<210> 415
<211> 217
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(217)
<223> n = A,T,C or G

<400> 415
gcataggatt aagactgagt atcttttcta cattctttta actttctaag gggcacttct 60
caaaacacag accaggtagc aaatctccac tgctctaagg ntctcaccac cactttctca 120
cacctagcaa tagtagaatt cagtcctact tctgaggcca gaagaatggt tcagaaaaat 180
antggattat aaaaaataac aattaagaaa aataatc 217

<210> 416
<211> 213
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(213)
<223> n = A,T,C or G

<400> 416
atgcataatnt aaagganact gcctcgcttt tagaagacat ctggngctgct ctctgcatga 60
ggcacagcag taaagctctt tgattcccag aatcaagaac tctccccttc agactattac 120
cgaatgcaag gtgggttaatt gaaggccact aattgatgct caaatagaag gatattgact 180
atattggaac agatggagtc tctactacaa aag 213

<210> 417
<211> 303
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(303)
<223> n = A,T,C or G

<400> 417
nagtcttcag gccatcagg gaagttcaca ctggagagaa gtcatacata tgtactgtat 60

134

```

gtgggaaagg ctttactctg agttcaaadc ttcaagccca tcagagagtc cactctggag 120
agaagccata caaatgcaat gagggtggga agagcttcag gagggtattcc cattatcaag 180
ttcatctagt ggtccacaca ggagagaaac cctataaatg tgagatatgt gggaagggct 240
tcantcaaag ttcgtatctt caaatccatc ngaaggncca cagtatanan aaacctttta 300
agt 303

```

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<210> 418
<211> 328
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)...(328)
<223> n = A,T,C or G

```

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<400> 418
tttttgccgg tgggtggggca gggacggggac angagtctca ctctgttgcc caggctggag 60
tgcacaggca tgatctcggc tcaactacaac ccctgcctcc catgtccaag cgattcttgt 120
gcctcagcct tccctgtagc tagaattaca ggcacatgcc accacaccca gctagttttt 180
gtatttttag tagagacagg gtttcacccat gttggccagg ctggtctcaa actcctnacc 240
tcagnggtca ggctggtctc aaactcctga cctcaagtga tctgccacc tcagcctccc 300
aaagtgtan gattacaggc cgtgagcc 328

```

```

<210> 419
<211> 389
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(389)
<223> n = A,T,C or G

```

```

<400> 419
cctcctcaag acggcctgtg gtccgcctcc cggcaaccaa gaagcctgca gtgccatatg 60
accctgagc catggactgg agcctgaaag gcagcgtaca ccctgctcct gatcttgctg 120
cttgcttctc ctctgtggct ccattcatag cacagttgtt gactgaggc ttgtgcaggc 180
cgagcaaggc caagctggct caaagagcaa ccagtcaact ctgccacggg gtgccaggca 240
ccgttctctc agccaccaac ctcaactcgt cccgcaaatg gcacatcagt tcttctaccc 300
taaaggtagg accaaagggc atctgctttt ctgaagtcct ctgctctatc agccatcacg 360
tggcagccac tcnggctgtg tcgacgcgg 389

```

```

<210> 420
<211> 408
<212> DNA
<213> Homo sapiens

```

```

<400> 420
gttctccta actcctgcca gaaacagctc tctcaacat gagagctgca cccctcctcc 60
tggccagggc agcaagcctt agccttggtt tcttgcttct gcttttttcc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgactttggt gtttcggcat ggagaccgaa 180
gtcccattga cactttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcttgaat gagtctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg aagtgcctatg acaaacctgg caagcccg 408

```

```

<210> 421
<211> 352
<212> DNA
<213> Homo sapiens

```

135

<220>
 <221> misc_feature
 <222> (1)...(352)
 <223> n = A,T,C or G

<400> 421
 gctcaaaaat ctttttactg atnggcatgg ctacacaatc attgactatt acggaggcca 60
 gaggagaatg aggcctggcc tgggagccct gtgcctacta naagcacatt agattatcca 120
 ttcactgaca gaacaggtct tttttgggtc cttcttctcc accacnatac acttgcaatc 180
 ctccctcttg aagattcttt ggcagttgtc tttgtcataa cccacaggtg tagaaacaag 240
 ggtgcaacat gaaatttctg tttcgtagca agtgcattgc tcacaagttg gcangtctgc 300
 cactccgagt ttattgggtg tttgtttcct ttgagatcca tgcatttcct gg 352

<210> 422
 <211> 337
 <212> DNA
 <213> Homo sapiens

<400> 422
 atgccaccat gctggcaatg cagcgggagg tcgaaggcct gcatatccag cccaagctgg 60
 cgatgatcga cggcaaccgt tgcccgaagt tgccgatgcc agccgaagcg gtggtcaagg 120
 gcgatagcaa ggtgccggcg atcgcgggcg cgtcaatcct ggccaaggct agccgtgatc 180
 gtgaaatggc agctgtcgaa ttgatctacc cgggttatgg catcgggcgg cataagggtc 240
 atccgacacc ggtgcacctg gaagccttgc agcggctggg gccgacgccg attcaccgac 300
 gcttcttccg ccggtacggc tggcctatga aaattat 337

<210> 423
 <211> 310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(310)
 <223> n = A,T,C or G

<400> 423
 gctcaaaaat ctttttactg atatggcatg gctacacaat cattgactat tagaggccag 60
 aggagaatga ggcctggcct gggagccctg tgcctactan aagcncatta gattatccat 120
 ttcactgacag aacaggtctt ttttgggtcc ttcttctcca ccacgatata cttgcagtcc 180
 tccttcttga agattctttg gcagttgtct ttgtcataac ccacaggtgt anaaacaagg 240
 gtgcaacatg aaatttctgt ttcgtagcaa gtgcattgtc cacagttgtc aagtctgccc 300
 tccgagttta 310

<210> 424
 <211> 370
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(370)
 <223> n = A,T,C or G

<400> 424
 gctcaaaaat ctttttactg ataggcatgg ctacacaatc attgactatt agaggccaga 60
 ggagaatgag gcctggcctg ggagccctgt gcctactaga agcacattag attatccatt 120
 cactgacaga acaggtcttt tttgggtcct tcttctccac cacgatatac ttgcagtctc 180
 ccttcttgaa gattcttttg cagttgtctt tgtcataacc cacaggtgta gaaacatcct 240
 gggtgaatct cctggaactc cctcattagg tatgaaatag catgatgcat tgcataaagt 300
 cacgaagggt gcaaagatca caacgctgcc cagganaaca ttcattgtga taagcaggac 360
 tccgtcgacg 370

136

<210> 425
 <211> 216
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(216)
 <223> n = A,T,C or G

<400> 425
 aattgctatn ntttattttg ccactcaaaa taattaccaa aaaaaaaaaa tnttaaata 60
 taacaacnca acatcaaggn aaananaaca ggaatggntg actntgcata aatnggccga 120
 anattatcca ttatnttaag gggtgacttc aggnacagc acacagacaa acatgcccag 180
 gaggnntntca ggaccgctcg atgtntnttg aggagg 216

<210> 426
 <211> 596
 <212> DNA
 <213> Homo sapiens

<400> 426
 cttccagtga ggataaccct gttgccccgg gccgagggtc tccattaggc tctgattgat 60
 tggcagtcag tgatggaagg gtgttctgat cattccgact gccccaaggg tcgctggcca 120
 gctctctgtt ttgctgagtt ggcagtagga cctaatttgt taattaagag tagatgggtga 180
 gctgtccttg tattttgatt aacctaatgg ccttcccagc acgactcgga ttcagctgga 240
 gacatcacgg caacttttaa tgaaatgatt tgaagggcca ttaagaggca cttcccgtta 300
 ttaggcagtt catctgact gataacttct tggcagctga gctggtcgga gctgtggccc 360
 aaacgcacac ttggcttttg gttttgagat acaactctta atcttttagt catgcttgag 420
 ggtggatggc cttttcagct ttaacccaat ttgcaactgcc ttggaagtgt agccaggaga 480
 atacactcat atactcgtgg gcttagaggc cacagcagat gtcattggc tactgcctga 540
 gtcccgtctg tcccatccca ggaccttcca tcggcgagta cctgggagcc cgtgct 596

<210> 427
 <211> 107
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(107)
 <223> n = A,T,C or G

<400> 427
 gaagaattca agtttagttt attcaaaggg cttacngaga atcctanacc caggncccag 60
 cccgggagca gccttanaga gctcctgttt gactgcccgg ctcagng 107

<210> 428
 <211> 38
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(38)
 <223> n = A,T,C or G

<400> 428
 gaacttcna anaangactt tattcactat tttacatt

38

<210> 429

137

<211> 544
<212> DNA
<213> Homo sapiens

<400> 429
ctttgctgga cggaataaaa gtggacgcaa gcatgacctc ctgatgaggg cgctgcattt 60
attgaagagc ggctgcagcc ctgcggttca gattaaaatc cgagaattgt atagacgccg 120
atatccacga actcttgaag gactttctga tttatccaca atcaaatcat cggttttcag 180
tttgatgggt ggctcatcac ctgtagaacc tgacttggcc gtggctggaa tccactcggt 240
gccttccact tcagttacac ctcactcacc atcctctcct gttggttctg tgctgcttca 300
agatactaag cccacatttg agatgcagca gccatctccc ccaattcttc ctgtccatcc 360
tgatgtgcag ttaaaaaatc tgccctttta tgatgtcctt gatgttctca tcaagcccac 420
gagtttagtt caaagcagta ttcagcgatt tcaagagaag ttttttattt ttgctttgac 480
acctcaacaa gtttagagaga tatgcatatc cagggatttt ttgccagggt gtaggagaga 540
ttat 544

<210> 430
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(507)
<223> n = A,T,C or G

<400> 430
cttatcncaa tgggggtccc aaacttggct gtgcagtgga aactccgggg gaattttgaa 60
gaacactgac acccatcttc caccocgaca ctctgattta attgggctgc agtgagaaca 120
gagcatcaat ttaaaaagct gcccagaatg ttntcctggg cagcgttggt atctttgccn 180
ccttcgtgac tttatgcaat gcatcatgct atttcatacc taatgaggga gttccaggag 240
attcaaccag gatgtttcta cncctgtggg ttatgacaaa gacaactgcc aaagaatntt 300
caagaaggag gactgcaagt atatcggtgt ggagaagaag gacccaaaaa agacctgttc 360
tgtcagtga tggataatct aatgtgcttc tagtaggcac agggctocca ggccaggcct 420
cattctcctc tggcctctaa tagtcaatga ttgtgtagcc atgcctatca gtaaaaagat 480
ttttgagcaa aaaaaaaaaa aaaaaaa 507

<210> 431
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(392)
<223> n = A,T,C or G

<400> 431
gaaaattcag aatggataaa aacaaatgaa gtacaaaata tttcagattt acatagcgat 60
aaacaagaaa gcacttatca ggaggactta caaatggaag tacactctan aaccatcatc 120
tatcatggct aaatgtgaga ttagcacagc tgtattattt gtacattgca aacacctaga 180
aagagatggg aaacaaaatc ccaggagttt tgtgtgtgga gtctggggtt ttccaacaga 240
catcattcca gcattctgag attagggnga ttggggatca ttctggagtt ggaatgttca 300
acaaaagtga tggtgttagg taaaatgtac aactctctga tctatgcaga cattgaaggt 360
gcaatgagtc tggcttttac tctgctgttt ct 392

<210> 432
<211> 387
<212> DNA
<213> Homo sapiens

<220>

138

<221> misc_feature
<222> (1)...(387)
<223> n = A,T,C or G

<400> 432
ggtatccnta cataatcaaa tatagctgta gtacatgttt tcattggngt agattaccac 60
aaatgcaagg caacatgtgt agatctcttg tcttattctt ttgtctataa tactgtattg 120
ngtagtccaa gctctcggna gtccagccac tngaaacat gctcccttta gattaacctc 180
gtggacnctn ttgttgnatt gtctgaactg tagngccctg tattttgctt ctgtctgnga 240
attctgttgc ttctggggca tttccttgng atgcagagga ccaccacaca gatgacagca 300
atctgaattg ntccaatcac agctgcgatt aagacatact gaaatcgtac aggaccggga 360
acaacgtata gaacactgga gtccctt 387

<210> 433
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(281)
<223> n = A,T,C or G

<400> 433
ttcaactagc anagaanact gcttcagggn gtgtaaaatg aaaggcttcc acgcagttat 60
ctgattaaag aacactaaga gagggacaag gctagaagcc gcaggatgtc tacactatag 120
caggcnctat ttgggttggc tggaggagct gtggaaaaca tggagagatt ggcgctggag 180
atcgccgtgg ctattcctcn ttgntattac accagngagg ntctctgtnt gccactggt 240
tnnaaaaccg ntatacaata atgatagaat aggacacaca t 281

<210> 434
<211> 484
<212> DNA
<213> Homo sapiens

<400> 434
ttttaaaata agcatttagt gctcagtcct tactgagtac tctttctctc ccctcctctg 60
aatttaattc tttcaacttg caatttgcaa ggattacaca tttcactgtg atgtatattg 120
tgttgcaaaa aaaaaaaagt gtctttgttt aaaattactt ggtttgtgaa tccatcttgc 180
tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa acatctgaag 240
agctagtcta tcagcatctg acaggtgaat tggatgggtc tcagaacat ttcaccaga 300
cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca taacaaaccc 360
tgctccaatc tgtcacataa aagtctgtga cttgaagttt agtcagcacc cccaccaaac 420
tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataaag taccatgtc 480
ttaa 484

<210> 435
<211> 424
<212> DNA
<213> Homo sapiens

<400> 435
gcgccgtca gagcaggtca ctttctgcct tccacgtcct ccttcaagga agccccatgt 60
gggtagcttt caatatcgca ggttcttact cctctgcctc tataagctca aaccaccaa 120
cgatcgggca agtaaacccc ctccctcgcc gacttcggaa ctggcgagag ttcagcgag 180
atgggcctgt ggggagggg caagatagat gagggggagc ggcatggtgc ggggtgaccc 240
cttgagagaga ggaaaaaggc cacaagaggg gctgccaccg ccactaacgg agatggccct 300
ggtagagacc tttgggggtc tggaaacctc ggactcccca tgccttaact cccacactct 360
gctatcagaa acttaaaactt gaggattttc tctgtttttc actcgcaata aattcagagc 420
aaac 424

<210> 436

<211> 667
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(667)
<223> n = A,T,C or G

<400> 436
accttgggaa nactctcaca atataaaggg tcgtagactt tactccaaat tccaaaaagg 60
tcctggccat gtaatcctga aagttttccc aaggtagcta taaaatcctt ataaggggtgc 120
agcctcttct ggaattcctc tgattttcaaa gtctcactct caagttcttg aaaacgaggg 180
cagttcctga aaggcaggta tagcaactga tcttcagaaa gaggaactgt gtgcaccggg 240
atgggctgcc agagtaggat aggattccag atgctgacac cttctggggg aaacagggct 300
gccaggtttg tcatagcact catcaaagtc cgggtcaacgt ctgtgcttcg aatataaacc 360
tgttcatgtt tataggactc attcaagaat tttctatata tctttcttat atactctcca 420
agttcataat gctgctccat gccagctgg gtgagttggc caaatccttg tggccatgag 480
gattccttta tggggctcagt gggaaagggt tcaatgggac ttcggtctcc atgccgaaac 540
accaaagtc acaacttcaa ctcttggt agtacacttc ggtctagcca gaaaaaagg 600
agaaacaaga agccaaggct aaggcttgct gcctgccag gaggaggggt gcagctctca 660
tgttgag 667

<210> 437
<211> 693
<212> DNA
<213> Homo sapiens

<400> 437
ctacgtctca accctcattt ttaggtaagg aatcttaagt ccaaagatat taagtgactc 60
acacagccag gtaaggaaag ctggattggc acactaggac tctaccatac cgggttttgt 120
taaagctcag gttaggaggc tgataagctt ggaaggaaact tcagacagct ttttcagatc 180
ataaaagata attcttagcc catgttcttc tccagagcag acctgaaatg acagcacagc 240
aggtaactct ctattttcac cctctttgct tctactctct ggcagtcaga cctgtgggag 300
gccatgggag aaagcagctc tctggatgtt tgtacagatc atggactatt ctctgtggac 360
catttctcca ggttacccta ggtgtcacta ttggggggac agccagcatc tttagctttc 420
atttgagttt ctgtctgtct tcagtagagg aaacttttgc tcttcacact tcacatctga 480
acacctaaact gctgttgctc ctgaggtggg gaaagacaga tatagagctt acagtattta 540
tcctatttct aggcactgag ggctgtgggg taccttgggg tgccaaaaca gatcctgttt 600
taaggacatg ttgcttcaga gatgtctgta actatctggg ggctctgttg gctctttacc 660
ctgcatcatg tgctctcttg gctgaaaatg acc 693

<210> 438
<211> 360
<212> DNA
<213> Homo sapiens

<400> 438
ctgcttatca caatgaatgt tctcctgggc agcgttgtga tctttgccac ctctgtgact 60
ttatgcaatg catcatgcta tttcatacct aatgaggag ttccaggaga ttcaaccagg 120
atgtttctac acctgtgggt tatgacaaag acaactgcc aagaatcttc aagaaggagg 180
actgcaagta tatctggtgg agaagaagga cccaaaaaag acctgttctg tcagtgaatg 240
gataatctaa tgtgcttcta gtaggcacag ggctcccagg ccaggcctca ttctcctctg 300
gcctctaata gtcaataatt gtgtagccat gcctatcagt aaaaagattt ttgagcaaac 360

<210> 439
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

140

<222> (1)...(431)

<223> n = A,T,C or G

<400> 439

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gttcctnnta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tgccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcctgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag t                                     431

```

<210> 440

<211> 523

<212> DNA

<213> Homo sapiens

<400> 440

```

agagataaag cttaggtcaa agttcataga gttcccatga actatatgac tggccacaca 60
ggatcttttg tatttaagga ttctgagatt ttgcttgagc aggattagat aaggctgttc 120
tttaaatgtc tgaaatggaa cagatttcaa aaaaaaaccc cacaatctag ggtgggaaca 180
aggaaggaaa gatgtgaata ggctgatggg caaaaaacca atttaccat cagttccagc 240
cttctctcaa ggagaggcaa agaaaggaga tacagtggag acatctggaa agttttctcc 300
actggaaaac tgctactatc tgtttttata tttctgttaa aatatatgag gctacagaac 360
taaaaattaa aacctctttg tgtcccttgg tcctggaaca tttatgttcc ttttaaagaa 420
acaaaaatca aactttacag aaagatttga tgtatgtaac acatatagca gctcttgaag 480
tatatatatc atagcaaata agtcatctga tgagaacaag cta                                     523

```

<210> 441

<211> 430

<212> DNA

<213> Homo sapiens

<400> 441

```

gttcctccta actcctgcc aaaaacagctc tcctcaacat gagagctgca cccctcctcc 60
tgccagggc agcaagcctt agccttggct tcttgtttct gctttttttc tggctagacc 120
gaagtgtact agccaaggag ttgaagtttg tgacttttgt gtttcggcat ggagaccgaa 180
gtcccattga cacctttccc actgacccca taaaggaatc ctcatggcca caaggatttg 240
gccaactcac ccagctgggc atggagcagc attatgaact tggagagtat ataagaaaga 300
gatatagaaa attcctgaat gagtcctata aacatgaaca ggtttatatt cgaagcacag 360
acgttgaccg gactttgatg agtgctatga caaacctggc agcccgtcga cgcggccgcg 420
aatttagtag                                     430

```

<210> 442

<211> 362

<212> DNA

<213> Homo sapiens

<400> 442

```

ctaaggaatt agtagtggtc ccatcacttg tttggagtgt gctattctaa aagattttga 60
tttcctggaa tgacaattat attttaactt tgggtgggga aagagttata ggaccacagt 120
cttcacttct gatacttgta aattaactct ttattgcact tgttttgacc attagctat 180
atgttttagaa atggtcattt tacggaaaaa ttagaaaaat tctgataata gtgcagaata 240
aatgaattaa tgttttactt aatttatatt gaactgtcaa tgacaaataa aaattctttt 300
tgattatttt ttgttttcat ttaccagaat aaaaactaag aattaaaagt ttgattacag 360
tc                                     362

```

<210> 443

<211> 624

<212> DNA

<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(624)
<223> n = A,T,C or G

<400> 443
tttttttttt gcaacacaat atacatcaca gtgaaatgtg taatccttgc aaattgcaag 60
ttgaaagaat taaattcaga ggaggggaga gaaagagtag tcagtaggga ctgagcacta 120
aatgcttatt ttaaaagaaa tgtaaagagc agaaagcaat tcaggctacc ctgccttttg 180
tgctggctag tactccggtc ggtgtcagca gcacgtggca ttgaacattg caatgtggag 240
cccaaaccac agaaaatggg gtgaaattgg ccaactttct attaacttgg cttoctgttt 300
tataaaatat tgtgaataat atcacctact tcaaagggca gttatgaggc ttaaataaac 360
taacgcctac aaaacactta aacatagata acataggtgc aagtactatg tatctggtac 420
atggtaaaca tccttattat taaagtcaac gctaaaatga atgtgtgtgc atatgctaata 480
agtacagaga gagggcactt aaaccaacta agggcctgga gggaagggtt cctggaaaga 540
ngatgcttgt gctgggtcca aatcttggtc tactatgacc ttggccaaat tatttaaact 600
ttgtccctat ctgctaaaca gatc 624

<210> 444
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(425)
<223> n = A,T,C or G

<400> 444
gcacatcatt nntcttgcatt tctttgagaa taagaagatc agtaaatagt tcagaagtgg 60
gaagctttgt ccaggcctgt gtgtgaaccc aatgttttgc ttagaaatag aacaagtaag 120
ttcattgcta tagcataaca caaaatttgc ataagtggtg gtcagcaaat ccttgaatgc 180
tgcttaattg gagaggttgg taaaatcctt tgtgcaacac tctaactccc tgaatgtttt 240
gctgtgctgg gacctgtgca tgccagacaa ggccaagctg gctgaaagag caaccagcca 300
cctctgcaat ctgccacctc ctgctggcag gatttgtttt tgcactcctg gaagagccaa 360
ggaggcacca gggcataagt gagtagactt atggtcgacg cggccgcgaa ttagtagta 420
gtaga 425

<210> 445
<211> 414
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(414)
<223> n = A,T,C or G

<400> 445
catgtttatg nttttggatt actttgggca cctagtgttt ctaaatcgtc tatcattctt 60
ttctgttttt caaaagcaga gatggccaga gtctcaacaa actgtatctt caagtctttg 120
tgaaattctt tgcattgtggc agattatttg atgtagtctt cttaactag catataaatc 180
tggtgtgttt cagataaatg aacagcaaaa tgtggtggaa ttaccatttg gaacattgtg 240
aatgaaaaat tgtgtctcta gattatgtaa caaataacta tttcctaacc attgatcttt 300
ggatttttat aatcctactc acaaatgact aggcttctcc tcttgtattt tgaagcagtg 360
tgggtgctgg attgataaaa aaaaaaaaaa tcgacgcggc cgcaattta gtag 414

<210> 446
<211> 631
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(631)
<223> n = A,T,C or G

<400> 446
acaaattaga anaaagtgcc agagaacacc acataccttg tccggaacat tacaatggct 60
tctgcatgca tgggaagtgt gagcattcta tcaatatgca ggagccatct tgcagggtgtg 120
atgctgggta tactggacaa cactgtgaaa aaaaggacta cagtgttcta tacgttggtc 180
ccggtcctgt acgatttcag tatgtcttaa tcgcagctgt gattggaaca attcagattg 240
ctgtcatctg tgtgggtggtc ctctgcatca caagggccaa actttaggta atagcattgg 300
actgagattt gtaaactttc caaccttcca ggaaatgccc cagaagcaac agaattcaca 360
gacagaagca aaatacaggg cactacagtt cagacaatac aacaagagcg tccacgaggt 420
taatctaaag ggagcatgtt tcacagtggc tggactaccg agagcttggg ctacacaata 480
cagtattata gacaaaagaa taagacaaga gatctacaca tgttgcttg catttggtgtg 540
aatctacacc aatgaaaaca tgtactacag ctatatattga ttatgtatgg atatatttga 600
aatagtatac attgtcttga tgttttttct g 631

<210> 447
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(585)
<223> n = A,T,C or G

<400> 447
ccttgggaaa antntcacaa tataaagggt cgtagacttt actccaaatt ccaaaaaggt 60
cctggccatg taatcctgaa agttttccca aggtagctat aaaatcctta taaggggtgca 120
gcctcttctg gaattcctct gatttcaaag tctcactctc aagtcttga aaacgagggc 180
agttcctgaa aggcaggtat agcaactgat cttcagaaaag aggaactgtg tgcaccggga 240
tgggctgcca gagtaggata ggattccaga tgctgacacc ttctggggga aacagggctg 300
ccaggtttgt catagcactc atcaaagtcc ggtcaacgtc tgtgcttcga atataaacct 360
gttcatgttt ataggactca ttcaagaatt ttctatatct ctttcttata tactctccaa 420
gttcataatg ctgctccatg cccagctggg tgagttggcc aaatccttgt ggccatgagg 480
attcctttat ggggtcagtg ggaaagggtg caatgggact tcggtctcca tgccgaaaca 540
ccaaagtcac aaacttcaac tccttggtca gtacacttcg gtcta 585

<210> 448
<211> 93
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(93)
<223> n = A,T,C or G

<400> 448
tgctcgtggg tcattctgan nnccgaactg accntgccag ccctgccgan ggccnccat 60
ggctccctag tgccctggag agganggggc tag 93

<210> 449
<211> 706
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature

<222> (1)...(706)

<223> n = A,T,C or G

<400> 449

```

ccaagtcat gctntgtgct ggacgctgga caggggggcaa aagcnnttgc tcgtgggtca 60
ttctgancac cgaactgacc atgccagccc tgccgatggt cctccatggc tccctagtgc 120
cctggagagg aggtgtctag tcagagagta gtccctggaag gtggcctctg ngaggagcca 180
cggggacagc atcctgcaga tggctggggcg cgtcccattc gccattcagg ctgcgcaact 240
gttgggaagg gcgatcggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 300
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcncga cgttgtaaaa 360
cgacggccag tgaattgaat ttaggtgacn ctatagaaga gctatgacgt cgcagtcacg 420
cgtacgtaag ctgggaccc cttagagcggc cgccactac tactaaattc gcggccgcgt 480
cgacgtggga tccnccactga gagagtggag agtgacatgt gctggacnct gtccatgaag 540
cactgagcag aagctggagg cacaacgcnc cagacactca cagctactca ggaggctgag 600
aacaggttga acctgggagg tggaggttgc aatgagctga gatcaggccn ctgcncccca 660
gcatggatga cagagtgaaa ctccatctta aaaaaaaaaa aaaaaa 706

```

<210> 450

<211> 493

<212> DNA

<213> Homo sapiens

<400> 450

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gagacggagt gtcactctgt tgcccaggct ggagtgcagc aagacactgt ctaagaaaaa 60
acagttttta aaggtaaaac aacataaaaa gaaatatacct atagtggaaa taagagagtc 120
aaatgaggct gagaacttta caaagggatc ttacagacat gtcgccaata tcaactgcatg 180
agcctaagta taagaacaac ctttggggag aaaccatcat ttgacagtga ggtacaattc 240
caagtcagggt agtgaatgg gtggaattaa actcaaatta atcctgccag ctgaaacgca 300
agagacactg tcagagagtt aaaaagtggg ttctatccat gaggtgattc cacagtcttc 360
tcaagtcacac acatctgtga actcacagac caagttctta aaccactgtt caaactctgc 420
tacacatcag aatcacctgg agagctttac aaactcccat tgccgagggg cgacgcggcc 480
gcgaatttag tag 493

```

<210> 451

<211> 501

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(501)

<223> n = A,T,C or G

<400> 451

```

gggcgcgtcc cattcgccat tcaggctgcg caactgttgg gaagggcgat cgggtgcgggc 60
ctcttcgcta ttacgccagc tggcgaaagg gggatgtgct gcaagggcgat taagttgggt 120
aacgccaggg ttttcccagt cncgacgttg taaaacgacg gccagtgaat tgaatttagg 180
tgacnctata gaagagctat gacgtcgcat gcacgcgtac gtaagcttgg atcctctaga 240
gcggccgcct actactacta aattcgcggc cgcgtcgacg tgggatccnc actgagagag 300
tggagagtga catgtgctgg acnctgtcca tgaagcactg agcagaagct ggaggcacia 360
cgcncacagc actcacagct actcaggagg ctgagaacag gttgaacctg ggaggtggag 420
gttgcaatga gctgagatca ggccnctgcn cccagcatg gatgacagag tgaaactcca 480
tcttaaaaaa aaaaaaaaaa a

```

<210> 452

<211> 51

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<222> (1)...(51)

144

<223> n = A,T,C or G

<400> 452

agacggtttc accnttataaa cnccttttag gatgggnntt ggggagcaag c 51

<210> 453

<211> 317

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<222> (1)...(317)

<223> n = A,T,C or G

<400> 453

```
tacatcttgc tttttcccca ttggaactag tcattaaccc atctctgaac tggtagaaaa 60
acatctgaag agctagtcta tcagcatctg gcaagtgaat tggatgggtc tcagaaccat 120
ttcacccana cagcctgttt ctatcctgtt taataaatta gtttgggttc tctacatgca 180
taacaaaccc tgctccaatc tgtcacataa aagtctgtga cttgaagttt antcagcacc 240
cccaccaaac tttatttttc tatgtgtttt ttgcaacata tgagtgtttt gaaaataagg 300
taccatgtc tttatta 317
```

<210> 454

<211> 231

<212> DNA

<213> Homo sapiens

<400> 454

```
ttcgaggtag aatcaactct cagagtgtag tttccttcta tagatgagtc agcattaata 60
taagccacgc cagctctctg aaggagtctt gaattctcct ctgctcactc agtagaacca 120
agaagaccaa attcttctgc atcccagctt gcaaacaata ttgttcttct aggtctccac 180
ccttcctttt tcagtgttcc aaagctcctc acaatttcat gaacaacagc t 231
```

<210> 455

<211> 231

<212> DNA

<213> Homo sapiens

<400> 455

```
taccaagag ggcataataa tcagtctcac agtaggggtc accatcctcc aagtgaataa 60
cattgttccg aatgggcttt ccacaggcta cacacacaaa acaggaaaca tgccaagttt 120
gtttcaacgc attgatgact tctccaagga tcttcctttg gcatcgacca cattcagggg 180
caaagaattt ctcatagcac agctcacaat acagggtcctc tttctcctct a 231
```

<210> 456

<211> 231

<212> DNA

<213> Homo sapiens

<400> 456

```
ttggcaggta cccttataaa gaagacacca taccttatgc gttattaggt ggaataatca 60
ttccattcag tattatcggt attattcttg gagaaacct gtctgtttac tgtaaccttt 120
tgcaactcaa ttcctttatc aggaataact acatagccac tatttataaa gccattggaa 180
cctttttatt tgggtgcagct gctagtcagt ccctgactga cattgccaag t 231
```

<210> 457

<211> 231

<212> DNA

<213> Homo sapiens

<220>

145

<221> misc_feature
 <222> (1)...(231)
 <223> n = A,T,C or G

<400> 457
 cgaggtaccc aggggtctga aaatctctnn tttantagtc gatagcaaaa ttgttcatca 60
 gcattcctta atatgatctt gctataatta gatttttctc cattagagtt catacagttt 120
 tatttgattt tattagcaat ctctttcaga agacccttga gatcattaag ctttgtatcc 180
 agttgtctaa atcgatgcct catttcctct gaggtgtcgc tggcttttgt g 231

<210> 458
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 458
 aggtctggtt cccccactt ccaactcccct ctactctctc taggactggg ctgggcccaag 60
 agaagagggg tgggttaggga agccgttgag acctgaagcc ccaccctcta ccttccttca 120
 acaccctaac cttgggtaac agcatttgga attatcattt gggatgagta gaatttccaa 180
 ggtcctgggt taggcatttt gggggggccag accccaggag aagaagattc t 231

<210> 459
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 459
 ggtaccgagg ctgctgaca cagagaaaacc ccaacgcgag gaaaggaatg gccagccaca 60
 ccttcgcgaa acctgtggtg gcccaccagt cctaaccgga caggacagag agacagagca 120
 gccctgcact gttttccctc caccacagcc atcctgtccc tcattggctc tgtgctttcc 180
 actatacaca gtcaccgtcc caatgagaaa caagaaggag caccctccac a 231

<210> 460
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 460
 gcaggtataa catgctgcaa caacagatgt gactaggaac ggccggtgac atggggaggg 60
 cctatcacc ctttcttggg gggtgcttct tcacagtgat catgaagcct agcagcaaat 120
 cccacctccc cacacgcaca cggccagcct ggagcccaca gaagggtcct cctgcagcca 180
 gtggagcttg gtccagcctc cagtccaccc ctaccaggct taaggataga a 231

<210> 461
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 461
 cgaggtttga gaagctctaa tgtgcagggg agccgagaag caggcggcct agggagggtc 60
 gcgtgtgctc cagaagagt tgtgcatgcc agaggggaaa caggcgcctg tgtgtcctgg 120
 gtggggttca gtgaggagt ggaaattggt tcagcagaac caagccgttg ggtgaataag 180
 agggggattc catggcactg atagagccct atagtttcag agctgggaat t 231

<210> 462
 <211> 231
 <212> DNA
 <213> Homo sapiens

<400> 462
 aggtaccctc attgtagcca tgggaaaatt gatgttcagt ggggatcagt gaattaaatg 60
 gggtcatgca agtataaaaa ttaaaaaaaa aagacttcat gcccaatctc atatgatgtg 120

146

gaagaactgt tagagagacc aacagggtag tgggttagag atttccagag tcttacattt 180
tctagaggag gtatttaatt tcttctcact catccagtgt tgtatttagg a 231

<210> 463
<211> 231
<212> DNA
<213> Homo sapiens

<400> 463
tactccagcc tgggtgacaga gcgagaccct atcaccgccc cccaccccac caaaaaaaaaa 60
actgagtaga cagggtgtcct cttggcatgg taagtcttaa gtcccctccc agatctgtga 120
catttgacag gtgtcttttc ctctggacct cgggtgtccc atctgagtga gaaaaggcag 180
tggggagggtg gatcttccag tcgaagcggt atagaagccc gtgtgaaaag c 231

<210> 464
<211> 231
<212> DNA
<213> Homo sapiens

<400> 464
gtactctaag attttatcta agttgccttt tctgggtggg aaagtttaac cttagtgtact 60
aaggacatca catatgaaga atgtttaagt tggagggtggc aacgtgaatt gcaaacaggg 120
cctgcttcag tgactgtgtg cctgtagtcc cagctactcg ggagtctgtg tgaggccagg 180
ggtgccagcg caccagctag atgctctgta acttctaggc cccattttcc c 231

<210> 465
<211> 231
<212> DNA
<213> Homo sapiens

<400> 465
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<211> 231
<212> DNA
<213> Homo sapiens

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<213> Homo sapiens

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<211> 3112

<212> DNA

<213> Homo sapiens

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<210> 469

<211> 2229

<212> DNA

<213> Homo sapiens

<400> 469

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<211> 2426

<212> DNA

<213> Homo sapiens

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<211> 812

<212> DNA

<213> Homo sapiens

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<211> 515

<212> DNA

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150

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<210> 473

<211> 750

<212> PRT

<213> Homo sapiens

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Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala Phe Leu Asp Glu
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Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu Tyr Asn Phe Thr Gln Ile
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Pro His Leu Ala Gly Thr Glu Gln Asn Phe Gln Leu Ala Lys Gln Ile
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Tyr Asp Val Leu Leu Ser Tyr Pro Asn Lys Thr His Pro Asn Tyr Ile
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Phe Arg Gly Asn Lys Val Lys Asn Ala Gln Leu Ala Gly Ala Lys Gly
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Asn Ile Leu Asn Leu Asn Gly Ala Gly Asp Pro Leu Thr Pro Gly Tyr

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Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe	Lys	Tyr	His	Leu	Thr	Val
				565					570					575	
Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe	Glu	Leu	Ala	Asn	Ser	Ile	Val
			580					585					590		

152

Leu Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 595 600 605
 Asp Lys Ile Tyr Ser Ile Ser Met Lys His Pro Gln Glu Met Lys Thr
 610 615 620
 Tyr Ser Val Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn Phe Thr
 625 630 635 640
 Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe Asp Lys Ser
 645 650 655
 Asn Pro Ile Val Leu Arg Met Met Asn Asp Gln Leu Met Phe Leu Glu
 660 665 670
 Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg
 675 680 685
 His Val Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser
 690 695 700
 Phe Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp
 705 710 715 720
 Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala Ala
 725 730 735
 Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala
 740 745 750

<210> 474

<211> 386

<212> PRT

<213> Homo sapiens

<400> 474

Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala Ser Leu Ser Leu
 5 10 15
 Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg Ser Val Leu Ala
 20 25 30
 Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His Gly Asp Arg Ser
 35 40 45
 Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu Ser Ser Trp Pro
 50 55 60
 Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu Gln His Tyr Glu
 65 70 75 80
 Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe Leu Asn Glu Ser
 85 90 95
 Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp Val Asp Arg Thr
 100 105 110
 Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe Pro Pro Glu Gly
 115 120 125
 Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro Ile Pro Val His

153

130	135	140
Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu Pro Phe Arg Asn 145 150 155 160		
Cys Pro Arg Phe Gln Glu Leu Glu Ser Glu Thr Leu Lys Ser Glu Glu 165 170 175		
Phe Gln Lys Arg Leu His Pro Tyr Lys Asp Phe Ile Ala Thr Leu Gly 180 185 190		
Lys Leu Ser Gly Leu His Gly Gln Asp Leu Phe Gly Ile Trp Ser Lys 195 200 205		
Val Tyr Asp Pro Leu Tyr Cys Glu Ser Val His Asn Phe Thr Leu Pro 210 215 220		
Ser Trp Ala Thr Glu Asp Thr Met Thr Lys Leu Arg Glu Leu Ser Glu 225 230 235 240		
Leu Ser Leu Leu Ser Leu Tyr Gly Ile His Lys Gln Lys Glu Lys Ser 245 250 255		
Arg Leu Gln Gly Gly Val Leu Val Asn Glu Ile Leu Asn His Met Lys 260 265 270		
Arg Ala Thr Gln Ile Pro Ser Tyr Lys Lys Leu Ile Met Tyr Ser Ala 275 280 285		
His Asp Thr Thr Val Ser Gly Leu Gln Met Ala Leu Asp Val Tyr Asn 290 295 300		
Gly Leu Leu Pro Pro Tyr Ala Ser Cys His Leu Thr Glu Leu Tyr Phe 305 310 315 320		
Glu Lys Gly Glu Tyr Phe Val Glu Met Tyr Tyr Arg Asn Glu Thr Gln 325 330 335		
His Glu Pro Tyr Pro Leu Met Leu Pro Gly Cys Ser Pro Ser Cys Pro 340 345 350		
Leu Glu Arg Phe Ala Glu Leu Val Gly Pro Val Ile Pro Gln Asp Trp 355 360 365		
Ser Thr Glu Cys Met Thr Thr Asn Ser His Gln Gly Thr Glu Asp Ser 370 375 380		
Thr Asp 385		
<210> 475		
<211> 261		
<212> PRT		
<213> Homo sapiens		
<400> 475		
Met Trp Val Pro Val Val Phe Leu Thr Leu Ser Val Thr Trp Ile Gly 5 10 15		
Ala Ala Pro Leu Ile Leu Ser Arg Ile Val Gly Gly Trp Glu Cys Glu 20 25 30		

154

Lys His Ser Gln Pro Trp Gln Val Leu Val Ala Ser Arg Gly Arg Ala
 35 40 45
 Val Cys Gly Gly Val Leu Val His Pro Gln Trp Val Leu Thr Ala Ala
 50 55 60
 His Cys Ile Arg Asn Lys Ser Val Ile Leu Leu Gly Arg His Ser Leu
 65 70 75 80
 Phe His Pro Glu Asp Thr Gly Gln Val Phe Gln Val Ser His Ser Phe
 85 90 95
 Pro His Pro Leu Tyr Asp Met Ser Leu Leu Lys Asn Arg Phe Leu Arg
 100 105 110
 Pro Gly Asp Asp Ser Ser His Asp Leu Met Leu Leu Arg Leu Ser Glu
 115 120 125
 Pro Ala Glu Leu Thr Asp Ala Val Lys Val Met Asp Leu Pro Thr Gln
 130 135 140
 Glu Pro Ala Leu Gly Thr Thr Cys Tyr Ala Ser Gly Trp Gly Ser Ile
 145 150 155 160
 Glu Pro Glu Glu Phe Leu Thr Pro Lys Lys Leu Gln Cys Val Asp Leu
 165 170 175
 His Val Ile Ser Asn Asp Val Cys Ala Gln Val His Pro Gln Lys Val
 180 185 190...
 Thr Lys Phe Met Leu Cys Ala Gly Arg Trp Thr Gly Gly Lys Ser Thr
 195 200 205
 Cys Ser Gly Asp Ser Gly Gly Pro Leu Val Cys Asn Gly Val Leu Gln
 210 215 220
 Gly Ile Thr Ser Trp Gly Ser Glu Pro Cys Ala Leu Pro Glu Arg Pro
 225 230 235 240
 Ser Leu Tyr Thr Lys Val Val His Tyr Arg Lys Trp Ile Lys Asp Thr
 245 250 255
 Ile Val Ala Asn Pro
 260

<210> 476

<211> 1079

<212> PRT

<213> Homo sapiens

<400> 476

Met His His His His His His Met Trp Val Pro Val Val Phe Leu Thr
 5 10 15
 Leu Ser Val Thr Trp Ile Gly Ala Ala Pro Leu Ile Leu Ser Arg Ile
 20 25 30
 Val Gly Gly Trp Glu Cys Glu Lys His Ser Gln Pro Trp Gln Val Leu
 35 40 45

155

Val Ala Ser Arg Gly Arg Ala Val Cys Gly Gly Val Leu Val His Pro
 50 55 60
 Gln Trp Val Leu Thr Ala Ala His Cys Ile Arg Asn Lys Ser Val Ile
 65 70 75 80
 Leu Leu Gly Arg His Ser Leu Phe His Pro Glu Asp Thr Gly Gln Val
 85 90 95
 Phe Gln Val Ser His Ser Phe Pro His Pro Leu Tyr Asp Met Ser Leu
 100 105 110
 Leu Lys Asn Arg Phe Leu Arg Pro Gly Asp Asp Ser Ser His Asp Leu
 115 120 125
 Met Leu Leu Arg Leu Ser Glu Pro Ala Glu Leu Thr Asp Ala Val Lys
 130 135 140
 Val Met Asp Leu Pro Thr Gln Glu Pro Ala Leu Gly Thr Thr Cys Tyr
 145 150 155 160
 Ala Ser Gly Trp Gly Ser Ile Glu Pro Glu Glu Phe Leu Thr Pro Lys
 165 170 175
 Lys Leu Gln Cys Val Asp Leu His Val Ile Ser Asn Asp Val Cys Ala
 180 185 190
 Gln Val His Pro Gln Lys Val Thr Lys Phe Met Leu Cys Ala Gly Arg
 195 200 205
 Trp Thr Gly Gly Lys Ser Thr Cys Ser Gly Asp Ser Gly Gly Pro Leu
 210 215 220
 Val Cys Asn Gly Val Leu Gln Gly Ile Thr Ser Trp Gly Ser Glu Pro
 225 230 235 240
 Cys Ala Leu Pro Glu Arg Pro Ser Leu Tyr Thr Lys Val Val His Tyr
 245 250 255
 Arg Lys Trp Ile Lys Asp Thr Ile Val Ala Asn Pro Gly Ser Met Ala
 260 265 270
 Thr Ala Gly Asn Pro Trp Gly Trp Phe Leu Gly Tyr Leu Ile Leu Gly
 275 280 285
 Val Ala Gly Ser Leu Val Ser Gly Ser Cys Ser Gln Ile Ile Asn Gly
 290 295 300
 Glu Asp Cys Ser Pro His Ser Gln Pro Trp Gln Ala Ala Leu Val Met
 305 310 315 320
 Glu Asn Glu Leu Phe Cys Ser Gly Val Leu Val His Pro Gln Trp Val
 325 330 335
 Leu Ser Ala Ala His Cys Phe Gln Asn Ser Tyr Thr Ile Gly Leu Gly
 340 345 350
 Leu His Ser Leu Glu Ala Asp Gln Glu Pro Gly Ser Gln Met Val Glu
 355 360 365
 Ala Ser Leu Ser Val Arg His Pro Glu Tyr Asn Arg Pro Leu Leu Ala
 370 375 380

156

Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser Asp
 385 390 395 400
 Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly Asn
 405 410 415
 Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met Pro
 420' 425 430
 Thr Val Leu Gln Cys Val Asn Val Ser Val Val Ser Glu Glu Val Cys
 435 440 445
 Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala Gly
 450 455 460
 Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly Pro
 465 470 475 480
 Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys Ala
 485 490 495
 Pro Cys Gly Gln Val Gly Val Pro Gly Val Tyr Thr Asn Leu Cys Lys
 500 505 510
 Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Ala Ser Glu Phe Met Val
 515 520 525
 Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala Gln Leu
 530 535 540
 Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu Ala Ala
 545 550 555 560
 Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val Glu Glu
 565 570 575
 Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly Leu Val
 580 585 590
 Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly Arg Tyr
 595 600 605
 Gly Arg Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile Leu Leu
 610 615 620
 Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu Leu Cys
 625 630 635 640
 Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Leu Ile Leu Gly Val Gly
 645 650 655
 Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu Ala Leu
 660 665 670
 Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala Tyr Ser
 675 680 685
 Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr Leu Leu
 690 695 700
 Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu Gly Thr

705		710		715		720
Gln Glu Glu Cys	Leu Phe Gly Leu Leu Thr	Leu Ile Phe Leu Thr	Cys			
	725		730			735
Val Ala Ala Thr	Leu Leu Val Ala Glu Glu Ala Ala Leu Gly	Pro Thr				
	740		745			750
Glu Pro Ala Glu Gly	Leu Ser Ala Pro Ser Leu Ser	Pro His Cys Cys				
	755		760			765
Pro Cys Arg Ala Arg	Leu Ala Phe Arg Asn Leu Gly	Ala Leu Leu Pro				
	770		775			780
Arg Leu His Gln Leu Cys Cys Arg	Met Pro Arg Thr Leu Arg Arg	Leu				
	785		790			800
Phe Val Ala Glu	Leu Cys Ser Trp Met Ala Leu Met Thr	Phe Thr Leu				
	805		810			815
Phe Tyr Thr Asp	Phe Val Gly Glu Gly Leu Tyr Gln Gly	Val Pro Arg				
	820		825			830
Ala Glu Pro Gly Thr	Glu Ala Arg Arg His Tyr Asp	Glu Gly Val Arg				
	835		840			845
Met Gly Ser Leu Gly	Leu Phe Leu Gln Cys Ala Ile Ser Leu Val	Phe				
	850		855			860
Ser Leu Val Met Asp	Arg Leu Val Gln Arg Phe Gly Thr Arg	Ala Val				
	865		870			875
Tyr Leu Ala Ser	Val Ala Ala Phe Pro Val Ala Ala Gly	Ala Thr Cys				
	885		890			895
Leu Ser His Ser	Val Ala Val Val Thr Ala Ser Ala Ala	Leu Thr Gly				
	900		905			910
Phe Thr Phe Ser	Ala Leu Gln Ile Leu Pro Tyr Thr	Leu Ala Ser Leu				
	915		920			925
Tyr His Arg Glu Lys	Gln Val Phe Leu Pro Lys Tyr Arg Gly Asp Thr					
	930		935			940
Gly Gly Ala Ser Ser	Glu Asp Ser Leu Met Thr Ser Phe Leu Pro Gly					
	945		950			955
Pro Lys Pro Gly	Ala Pro Phe Pro Asn Gly His Val Gly	Ala Gly Gly				
	965		970			975
Ser Gly Leu Leu Pro	Pro Pro Pro Ala Leu Cys Gly Ala Ser	Ala Cys				
	980		985			990
Asp Val Ser Val Arg	Val Val Val Gly Glu Pro Thr Glu Ala Arg Val					
	995		1000			1005
Val Pro Gly Arg Gly	Ile Cys Leu Asp Leu Ala Ile Leu Asp Ser Ala					
	1010		1015			1020
Phe Leu Leu Ser Gln	Val Ala Pro Ser Leu Phe Met Gly Ser Ile Val					
	1025		1030			1035
						1040

158

Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala Gly Leu
1045 1050 1055

Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp Lys Ser
1060 1065 1070

Asp Leu Ala Lys Tyr Ser Ala
1075